

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 00:14:17 ; Search time 187 Seconds
(without alignments)
18.797 Million cell updates/sec

Title: US-10-748-765-2
Perfect score: 41
Sequence: 1 NAPVSIPQ 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	41	100.0	8	2	AAW64677	Aaw64677 Human ADN
	2	41	100.0	8	2	AAW64678	Aaw64678 Human ADN
	3	41	100.0	8	3	AAY71143	Aay71143 Human ADN
	4	41	100.0	8	3	AAB23470	Aab23470 Activity
	5	41	100.0	8	3	AAB23472	Aab23472 Activity
	6	41	100.0	8	4	AAB72322	Aab72322 Activity
	7	41	100.0	8	5	ABB07216	Abb07216 ADNF III
	8	41	100.0	8	6	ABR39742	Abr39742 ADNP I ac

9	41	100.0	8	7	ADA07953	Ada07953	Human act
10	41	100.0	8	8	ADQ76121	Adq76121	ADNF III
11	41	100.0	8	8	ADS73609	Ads73609	ADNF III
12	41	100.0	10	2	AAW64696	Aaw64696	Seq ID 33
13	41	100.0	10	3	AAY71139	Aay71139	Human Act
14	41	100.0	10	3	AAB23488	Aab23488	Activity
15	41	100.0	10	4	AAB72323	Aab72323	Activity
16	41	100.0	10	4	AAB72328	Aab72328	Activity
17	41	100.0	10	5	ABB07223	Abb07223	ADNF III
18	41	100.0	10	8	ADQ76135	Adq76135	ADNF III
19	41	100.0	10	8	ADQ76131	Adq76131	ADNF III
20	41	100.0	10	8	ADQ76137	Adq76137	ADNF III
21	41	100.0	10	8	ADS73616	Ads73616	ADNF III
22	41	100.0	10	8	ADS73620	Ads73620	ADNF III
23	41	100.0	13	2	AAW64697	Aaw64697	Seq ID 34
24	41	100.0	13	2	AAW64699	Aaw64699	Seq ID 36
25	41	100.0	13	3	AAB23489	Aab23489	Activity
26	41	100.0	13	4	AAB72324	Aab72324	Activity
27	41	100.0	13	5	ABB07224	Abb07224	ADNF III
28	41	100.0	13	8	ADQ76132	Adq76132	ADNF III
29	41	100.0	13	8	ADQ76122	Adq76122	ADNF III
30	41	100.0	13	8	ADS73632	Ads73632	Elongated
31	41	100.0	13	8	ADS73617	Ads73617	ADNF III
32	41	100.0	14	8	ADS73631	Ads73631	Elongated
33	41	100.0	15	2	AAW64698	Aaw64698	Seq ID 35
34	41	100.0	15	3	AAB23490	Aab23490	Activity
35	41	100.0	15	4	AAB72325	Aab72325	Activity
36	41	100.0	15	5	ABB07225	Abb07225	ADNF III
37	41	100.0	15	8	ADQ76123	Adq76123	ADNF III
38	41	100.0	15	8	ADQ76133	Adq76133	ADNF III
39	41	100.0	15	8	ADS73618	Ads73618	ADNF III
40	41	100.0	18	2	AAW64680	Aaw64680	Human ADN
41	41	100.0	18	3	AAY71145	Aay71145	Inactive
42	41	100.0	18	3	AAB23491	Aab23491	Activity
43	41	100.0	18	4	AAB72326	Aab72326	Activity
44	41	100.0	18	5	ABB07226	Abb07226	ADNF III
45	41	100.0	18	8	ADQ76134	Adq76134	ADNF III
46	41	100.0	18	8	ADQ76124	Adq76124	ADNF III
47	41	100.0	18	8	ADS73619	Ads73619	ADNF III
48	41	100.0	726	3	AAY71137	Aay71137	Human Act
49	41	100.0	781	2	AAW64695	Aaw64695	Mouse ADN
50	41	100.0	787	2	AAW64694	Aaw64694	Human ADN
51	41	100.0	800	2	AAW64703	Aaw64703	Seq ID 41
52	41	100.0	806	2	AAW64675	Aaw64675	Mouse ADN
53	41	100.0	806	3	AAY71135	Aay71135	Mouse Act
54	41	100.0	828	3	AAY71136	Aay71136	Mouse Act
55	41	100.0	874	3	AAY71138	Aay71138	Human Act
56	41	100.0	1000	2	AAW64674	Aaw64674	Human ADN
57	41	100.0	1000	3	AAY71134	Aay71134	Human Act
58	41	100.0	1069	7	ADA07959	Ada07959	Human act
59	41	100.0	1102	4	AAB31987	Aab31987	Human act
60	41	100.0	1102	4	AAM39291	Aam39291	Human pol
61	41	100.0	1102	4	ABB50198	Abb50198	Human tra
62	41	100.0	1102	7	ADA07951	Ada07951	Human act
63	41	100.0	1102	9	ADX06277	Adx06277	Cyclin-de
64	41	100.0	1154	4	AAM41077	Aam41077	Human pol
65	36	87.8	9	2	AAW64693	Aaw64693	Human ADN

66	36	87.8	9	3	AAy71157	Aay71157	Mouse	ADN
67	36	87.8	360	7	ABO83247	Abo83247	Pseudomon	
68	36	87.8	431	9	ADV16564	Adv16564	E. faecal	
69	36	87.8	466	5	ABP26208	Abp26208	Streptoco	
70	36	87.8	481	8	ADU69666	Adu69666	S agalact	
71	36	87.8	481	8	ADV89657	Adv89657	Streptoco	
72	36	87.8	481	8	ADV83059	Adv83059	Streptoco	
73	36	87.8	481	8	ADV80910	Adv80910	Streptoco	
74	36	87.8	510	4	AAU03127	Aau03127	Streptoco	
75	36	87.8	510	5	ABP29387	Abp29387	Streptoco	
76	36	87.8	510	6	ABU46653	Abu46653	Protein e	
77	36	87.8	510	6	ABU14609	Abu14609	Protein e	
78	36	87.8	510	8	ADI67150	Adi67150	Lactobaci	
79	36	87.8	511	6	ABU44144	Abu44144	Protein e	
80	36	87.8	519	7	ADH88341	Adh88341	Enterococ	
81	35	85.4	321	8	ADX96190	Adx96190	Plant ful	
82	35	85.4	331	4	ABB70820	Abb70820	Drosophil	
83	35	85.4	808	8	ADL33463	Adl33463	Festuca a	
84	35	85.4	3411	6	ABU33747	Abu33747	Protein e	
85	34	82.9	465	7	ABM89937	Abm89937	Rice abio	
86	34	82.9	469	6	ADA33535	Ada33535	Acinetoba	
87	34	82.9	505	4	ABB61600	Abb61600	Drosophil	
88	34	82.9	1301	2	AAW29115	Aaw29115	FMR2P pro	
89	33	80.5	78	8	ABO59158	Abo59158	Human gen	
90	33	80.5	108	4	AAO06996	Aao06996	Human pol	
91	33	80.5	205	7	ABO61031	Abo61031	Klebsiell	
92	33	80.5	295	6	ABU56250	Abu56250	Rat Neu1	
93	33	80.5	344	6	ABU56249	Abu56249	Rat Neu1	
94	33	80.5	344	6	ABU56246	Abu56246	Mouse Neu	
95	33	80.5	386	6	ABU56243	Abu56243	Human Neu	
96	33	80.5	386	8	ADQ15992	Adq15992	Human neu	
97	33	80.5	479	8	ADO02217	Ado02217	Thalecres	
98	33	80.5	481	7	ABO62631	Abo62631	Klebsiell	
99	33	80.5	546	2	AAy21559	Aay21559	Mouse ner	
100	33	80.5	557	6	ABU56245	Abu56245	Mouse Neu	
101	33	80.5	557	6	ABU56242	Abu56242	Human Neu	
102	33	80.5	557	6	AAO23972	Aao23972	Human neu	
103	33	80.5	574	2	AAy21558	Aay21558	Human ner	
104	33	80.5	574	6	ABU56241	Abu56241	Human Neu	
105	33	80.5	574	6	ABU56244	Abu56244	Mouse Neu	
106	33	80.5	574	6	ABU56248	Abu56248	Rat Neu1	
107	33	80.5	601	4	ABB59529	Abb59529	Drosophil	
108	33	80.5	1240	8	ADN21378	Adn21378	Bacterial	
109	32	78.0	67	5	ABP05693	Abp05693	Human ORF	
110	32	78.0	276	8	ADS29780	Ads29780	Bacterial	
111	32	78.0	394	6	ABU46426	Abu46426	Protein e	
112	32	78.0	468	3	AAG14350	Aag14350	Arabidops	
113	32	78.0	485	3	AAG14349	Aag14349	Arabidops	
114	32	78.0	622	8	ADS24400	Ads24400	Bacterial	
115	32	78.0	1015	4	ABB65826	Abb65826	Drosophil	
116	32	78.0	1414	7	ADD48516	Add48516	Rat Prote	
117	31	75.6	69	4	AAM14431	Aam14431	Peptide #	
118	31	75.6	69	4	ABB33379	Abb33379	Peptide #	
119	31	75.6	69	4	AAM26844	Aam26844	Peptide #	
120	31	75.6	69	4	ABB28204	Abb28204	Human pep	
121	31	75.6	69	4	ABB18838	Abb18838	Protein #	
122	31	75.6	69	4	AAM66558	Aam66558	Human bon	

123	31	75.6	69	4	AAM54164	Aam54164	Human bra
124	31	75.6	69	4	ABG48226	Abg48226	Human liv
125	31	75.6	69	4	AAM02158	Aam02158	Peptide #
126	31	75.6	69	5	ABG36210	Abg36210	Human pep
127	31	75.6	121	8	ADR08786	Adr08786	Human pro
128	31	75.6	123	7	ADM04853	Adm04853	Human pro
129	31	75.6	157	6	ABU31330	Abu31330	Protein e
130	31	75.6	159	6	ABU27389	Abu27389	Protein e
131	31	75.6	167	3	AAG59530	Aag59530	Arabidops
132	31	75.6	167	3	AAG55999	Aag55999	Arabidops
133	31	75.6	174	8	ADN27017	Adn27017	Bacterial
134	31	75.6	215	4	ABB60421	Abb60421	Drosophil
135	31	75.6	246	6	ABU44932	Abu44932	Protein e
136	31	75.6	292	6	ADA36770	Ada36770	Acinetoba
137	31	75.6	317	7	ADF04504	Adf04504	Bacterial
138	31	75.6	350	4	AAU38446	Aau38446	Salmonell
139	31	75.6	350	6	ABU47948	Abu47948	Protein e
140	31	75.6	350	6	ABU47193	Abu47193	Protein e
141	31	75.6	353	7	ADM04732	Adm04732	Human pro
142	31	75.6	354	6	ABU31806	Abu31806	Protein e
143	31	75.6	358	6	ABP80228	Abp80228	N. gonorr
144	31	75.6	373	8	ADX91193	Adx91193	Plant ful
145	31	75.6	373	8	ADX68491	Adx68491	Plant ful
146	31	75.6	373	8	ADX91607	Adx91607	Plant ful
147	31	75.6	376	7	ABO61018	Abo61018	Klebsiell
148	31	75.6	391	4	AAU34100	Aau34100	Staphyloc
149	31	75.6	392	2	AAY21893	Aay21893	PHA beta-
150	31	75.6	393	4	AAU36824	Aau36824	Staphyloc
151	31	75.6	393	6	ABU16102	Abu16102	Protein e
152	31	75.6	393	6	ABU35897	Abu35897	Protein e
153	31	75.6	393	6	ABM71709	Abm71709	Staphyloc
154	31	75.6	394	8	ADS21472	Ads21472	Bacterial
155	31	75.6	410	4	ABG23096	Abg23096	Novel hum
156	31	75.6	413	4	AAU60783	Aau60783	Propionib
157	31	75.6	413	6	ABM57302	Abm57302	Propionib
158	31	75.6	416	6	ABU19669	Abu19669	Protein e
159	31	75.6	421	2	AAR97602	Aar97602	Adenoviru
160	31	75.6	421	2	AAR97603	Aar97603	Adenoviru
161	31	75.6	421	2	AAR97594	Aar97594	Adenoviru
162	31	75.6	421	2	AAR97597	Aar97597	Adenoviru
163	31	75.6	421	2	AAR97599	Aar97599	Adenoviru
164	31	75.6	433	6	ABU31213	Abu31213	Protein e
165	31	75.6	444	9	ABM93179	Abm93179	M. xanthu
166	31	75.6	444	9	ADY64654	Ady64654	S. manson
167	31	75.6	445	6	ABU20061	Abu20061	Protein e
168	31	75.6	459	2	AAR08331	Aar08331	Hybrid mu
169	31	75.6	459	8	ADS85055	Ads85055	Mouse ato
170	31	75.6	459	9	ADZ13720	Adz13720	Murine ca
171	31	75.6	474	8	ADQ59427	Adq59427	Human can
172	31	75.6	481	7	ADM26462	Adm26462	Hyperther
173	31	75.6	518	6	ABJ19054	Abj19054	Pathogen
174	31	75.6	518	6	ABU42378	Abu42378	Protein e
175	31	75.6	518	6	ABM71299	Abm71299	Staphyloc
176	31	75.6	521	4	AAG81719	Aag81719	S. epider
177	31	75.6	521	6	ABU43291	Abu43291	Protein e
178	31	75.6	525	5	ABP38669	Abp38669	Staphyloc
179	31	75.6	525	8	ADS05182	Ads05182	Staphyloc

180	31	75.6	556	8	ADR09894	Adr09894	Human pro
181	31	75.6	558	9	AEB88782	Aeb88782	Cephalosp
182	31	75.6	558	9	AEB88784	Aeb88784	Cephalosp
183	31	75.6	573	7	ADD30652	Add30652	Plant yie
184	31	75.6	573	8	ADI44321	Adi44321	Plant tra
185	31	75.6	688	4	AAG91518	Aag91518	C glutami
186	31	75.6	836	4	ABB68208	Abb68208	Drosophil
187	31	75.6	880	4	AAB11485	Aab11485	Yeast Gal
188	31	75.6	881	2	AAW13082	Aaw13082	Yeast tra
189	31	75.6	881	2	AAW47124	Aaw47124	S. cerevi
190	31	75.6	881	5	AAU99987	Aau99987	Yeast GAL
191	31	75.6	881	5	ABP35637	Abp35637	Fungal ZB
192	31	75.6	881	8	ADM97772	Adm97772	Yeast Gal
193	31	75.6	881	8	ADN60221	Adn60221	S. cerevi
194	31	75.6	881	8	ADS44021	Ads44021	Bacterial
195	31	75.6	881	9	ADW86736	Adw86736	Yeast GAL
196	31	75.6	881	9	ADZ41461	Adz41461	Yeast GAL
197	31	75.6	882	2	AAR51930	Aar51930	Mutated G
198	31	75.6	917	6	AAO23321	Aao23321	Rhesus mo
199	31	75.6	926	9	AEB47203	Aeb47203	Chimpanze
200	31	75.6	930	9	AEB47180	Aeb47180	Chimpanze
201	31	75.6	930	9	AEB47181	Aeb47181	Chimpanze
202	31	75.6	932	6	AAO23299	Aao23299	Chimpanze
203	31	75.6	932	9	AEB47210	Aeb47210	Chimpanze
204	31	75.6	933	6	AAO23293	Aao23293	Chimpanze
205	31	75.6	933	6	ABP56651	Abp56651	Chimpanze
206	31	75.6	933	9	AEB47214	Aeb47214	Chimpanze
207	31	75.6	933	9	AEB47208	Aeb47208	Chimpanze
208	31	75.6	936	9	AEB47207	Aeb47207	Chimpanze
209	31	75.6	937	9	AEB47212	Aeb47212	Chimpanze
210	31	75.6	938	9	AEB47201	Aeb47201	Chimpanze
211	31	75.6	940	9	AEB47177	Aeb47177	Chimpanze
212	31	75.6	940	9	AEB47178	Aeb47178	Chimpanze
213	31	75.6	940	9	AEB47179	Aeb47179	Chimpanze
214	31	75.6	941	9	AEB47205	Aeb47205	Chimpanze
215	31	75.6	942	6	AAO23296	Aao23296	Chimpanze
216	31	75.6	942	9	AEB47209	Aeb47209	Chimpanze
217	31	75.6	944	9	AEB47183	Aeb47183	Chimpanze
218	31	75.6	946	9	AEB47193	Aeb47193	Chimpanze
219	31	75.6	952	2	AAW79539	Aaw79539	Adenoviru
220	31	75.6	952	2	AAW63118	Aaw63118	Human ade
221	31	75.6	954	9	AEB47176	Aeb47176	Chimpanze
222	31	75.6	954	9	AEB47191	Aeb47191	Chimpanze
223	31	75.6	956	9	AEB47213	Aeb47213	Chimpanze
224	31	75.6	956	9	AEB47189	Aeb47189	Chimpanze
225	31	75.6	958	9	AEB47185	Aeb47185	Chimpanze
226	31	75.6	958	9	AEB47197	Aeb47197	Chimpanze
227	31	75.6	960	9	AEB47182	Aeb47182	Chimpanze
228	31	75.6	960	9	AEB47184	Aeb47184	Chimpanze
229	31	75.6	960	9	AEB47211	Aeb47211	Chimpanze
230	31	75.6	968	2	AAW79538	Aaw79538	Adenoviru
231	31	75.6	1014	8	ADQ66671	Adq66671	Novel hum
232	31	75.6	1175	6	ABU29788	Abu29788	Protein e
233	31	75.6	1179	7	ADC96499	Adc96499	E. faeciu
234	31	75.6	1342	7	ADJ71015	Adj71015	Human hea
235	31	75.6	1344	8	ADO05306	Ado05306	Yeast int
236	31	75.6	1555	6	ABJ25640	Abj25640	Aspergill

237	31	75.6	1632	6	ABU21966	Abu21966	Protein e
238	31	75.6	1832	6	ABJ26240	Abj26240	Aspergill
239	31	75.6	1963	4	ABB62819	Abb62819	Drosophil
240	31	75.6	2512	6	ABU34845	Abu34845	Protein e
241	31	75.6	2512	6	ABU36419	Abu36419	Protein e
242	31	75.6	2517	9	ABM96181	Abm96181	M. xanthu
243	31	75.6	19938	6	ABP76682	Abp76682	Streptomy
244	30	73.2	12	9	ADV76253	Adv76253	Cancer di
245	30	73.2	15	9	ADW77821	Adw77821	Human can
246	30	73.2	18	2	AAW66395	Aaw66395	Cationic
247	30	73.2	18	2	AAW66396	Aaw66396	Cationic
248	30	73.2	18	2	AAW87604	Aaw87604	Antimicro
249	30	73.2	18	3	AAY44319	Aay44319	Antimicro
250	30	73.2	18	3	AAY91694	Aay91694	Cationic
251	30	73.2	18	3	AAY91769	Aay91769	Amino aci
252	30	73.2	18	3	AAY91695	Aay91695	Cationic
253	30	73.2	18	4	AAG62735	Aag62735	Amino aci
254	30	73.2	18	5	ABB81935	Abb81935	Peptide f
255	30	73.2	18	6	ADA00502	Ada00502	Antimicro
256	30	73.2	18	6	ABU59571	Abu59571	Cationic
257	30	73.2	18	6	ABU59572	Abu59572	Cationic
258	30	73.2	18	7	ADB81287	Adb81287	Biologica
259	30	73.2	18	7	ADC98849	Adc98849	Synthetic
260	30	73.2	18	8	ADD35366	Add35366	Antimicro
261	30	73.2	18	9	ADY67441	Ady67441	Tumor cel
262	30	73.2	18	9	ADY67440	Ady67440	Tumor cel
263	30	73.2	26	7	ADB81285	Adb81285	Biologica
264	30	73.2	47	4	AAM91313	Aam91313	Human imm
265	30	73.2	53	8	ABO57312	Abo57312	Human gen
266	30	73.2	55	5	ABP08508	Abp08508	Human ORF
267	30	73.2	55	5	ABP42161	Abp42161	Human ova
268	30	73.2	77	4	AAM95534	Aam95534	Human rep
269	30	73.2	77	4	ABB96216	Abb96216	Human tes
270	30	73.2	81	7	ADD35993	Add35993	Human DNA
271	30	73.2	90	4	AAG74248	Aag74248	Human col
272	30	73.2	98	2	AAW20312	Aaw20312	H. pylori
273	30	73.2	108	2	AAY09093	Aay09093	Human P-c
274	30	73.2	108	2	AAY17104	Aay17104	Human P-c
275	30	73.2	108	3	AAY78184	Aay78184	Human P-c
276	30	73.2	108	4	AAG65364	Aag65364	Human P-c
277	30	73.2	108	5	AAM47471	Aam47471	Human P-c
278	30	73.2	108	6	ABU60282	Abu60282	Human P-c
279	30	73.2	108	7	ABO43533	Abo43533	Human P-c
280	30	73.2	108	7	ABW01245	Abw01245	Human cad
281	30	73.2	108	8	ADK13538	Adk13538	Human P-c
282	30	73.2	108	8	ADO70610	Ado70610	Human E-c
283	30	73.2	108	9	ADX08225	Adx08225	Human P-c
284	30	73.2	108	9	AEB78127	Aeb78127	Human P-c
285	30	73.2	114	4	AAO02029	Aao02029	Human pol
286	30	73.2	118	2	AAW20868	Aaw20868	H. pylori
287	30	73.2	119	4	ABB64335	Abb64335	Drosophil
288	30	73.2	137	5	ABP64662	Abp64662	Human ORF
289	30	73.2	144	4	ABG30160	Abg30160	Novel hum
290	30	73.2	144	4	ABG05856	Abg05856	Novel hum
291	30	73.2	151	4	AAU22438	Aau22438	Human car
292	30	73.2	151	7	ADE46406	Ade46406	Human car
293	30	73.2	151	8	ADJ07824	Adj07824	Human car

294	30	73.2	158	4	ABG11679	Abg11679	Novel hum
295	30	73.2	159	7	ABM86654	Abm86654	Rice abio
296	30	73.2	161	4	ABG00722	Abg00722	Novel hum
297	30	73.2	163	2	AAY37682	Aay37682	Amino aci
298	30	73.2	171	7	ABO78677	Abo78677	Pseudomon
299	30	73.2	177	6	ABU39350	Abu39350	Protein e
300	30	73.2	198	8	ADN61437	Adn61437	Human KPP
301	30	73.2	201	4	AAM38762	Aam38762	Human pol
302	30	73.2	216	8	ABO84901	Abo84901	Human can
303	30	73.2	218	6	ADA09882	Ada09882	Human rec
304	30	73.2	221	4	ABG22964	Abg22964	Novel hum
305	30	73.2	221	4	ABG03524	Abg03524	Novel hum
306	30	73.2	221	4	ABG11678	Abg11678	Novel hum
307	30	73.2	238	3	AAB56789	Aab56789	Human pro
308	30	73.2	244	3	AAG38297	Aag38297	Arabidops
309	30	73.2	244	3	AAG07318	Aag07318	Arabidops
310	30	73.2	252	8	ADY11199	Ady11199	Plant ful
311	30	73.2	268	2	AAY36798	Aay36798	Protein i
312	30	73.2	268	3	AAG36834	Aag36834	Arabidops
313	30	73.2	269	3	AAG36833	Aag36833	Arabidops
314	30	73.2	274	8	ADY04858	Ady04858	Plant ful
315	30	73.2	276	4	AAU36083	Aau36083	Klebsiell
316	30	73.2	285	5	AAU93050	Aau93050	Arabidops
317	30	73.2	285	6	ADA15461	Ada15461	A. thalia
318	30	73.2	285	7	ADD30027	Add30027	Plant yie
319	30	73.2	285	8	ADI41763	Adi41763	Plant tra
320	30	73.2	285	8	ADO02313	Ado02313	Thalecres
321	30	73.2	285	8	ADQ16260	Adq16260	Thalecres
322	30	73.2	285	9	ADZ00598	Adz00598	G1075 pol
323	30	73.2	285	9	AEA26461	Aea26461	Stress to
324	30	73.2	297	7	ABO60872	Abo60872	Klebsiell
325	30	73.2	300	6	ABR52742	Abr52742	Protein s
326	30	73.2	300	7	ADK62038	Adk62038	Disease t
327	30	73.2	322	9	AEB91421	Aeb91421	Microbial
328	30	73.2	326	9	ADZ64850	Adz64850	Human pro
329	30	73.2	326	9	ADZ64848	Adz64848	Human pro
330	30	73.2	330	5	ABP65651	Abp65651	Bifidobac
331	30	73.2	332	3	AAG50741	Aag50741	Arabidops
332	30	73.2	332	3	AAG05112	Aag05112	Arabidops
333	30	73.2	342	8	ADN27274	Adn27274	Bacterial
334	30	73.2	350	9	ADZ64846	Adz64846	Human pro
335	30	73.2	358	4	ABB66830	Abb66830	Drosophil
336	30	73.2	362	3	AAG36832	Aag36832	Arabidops
337	30	73.2	364	9	ADV67459	Adv67459	Amino aci
338	30	73.2	365	6	ADA34820	Ada34820	Acinetoba
339	30	73.2	367	2	AAR63602	Aar63602	MAP-kinas
340	30	73.2	367	5	AAU84270	Aau84270	Human end
341	30	73.2	367	5	ABB82462	Abb82462	Human MAP
342	30	73.2	367	5	ABB57320	Abb57320	Mouse isc
343	30	73.2	367	5	ABP64714	Abp64714	Human pro
344	30	73.2	367	6	ABP96784	Abp96784	Human COP
345	30	73.2	367	6	ABR59708	Abr59708	Human dua
346	30	73.2	367	8	ADJ76316	Adj76316	Marker ge
347	30	73.2	367	8	ADJ75596	Adj75596	Marker ge
348	30	73.2	367	8	ADO60056	Ado60056	CRH signa
349	30	73.2	367	8	ADO19128	Ado19128	Human PRO
350	30	73.2	367	8	ADP23104	Adp23104	PRO polyp

351	30	73.2	367	8	ADR67291	Adr67291	Human bla
352	30	73.2	367	8	ADR96773	Adr96773	Human dua
353	30	73.2	367	9	ADY14384	Ady14384	PRO polyp
354	30	73.2	384	8	ADT58882	Adt58882	Plant pol
355	30	73.2	386	8	ABM84496	Abm84496	Human dia
356	30	73.2	388	3	AAB43313	Aab43313	Human ORF
357	30	73.2	395	6	ABU46749	Abu46749	Protein e
358	30	73.2	407	4	AAM93675	Aam93675	Human pol
359	30	73.2	407	8	ADL31531	Adl31531	Human pro
360	30	73.2	414	4	ABG08867	Abg08867	Novel hum
361	30	73.2	416	4	ABG22966	Abg22966	Novel hum
362	30	73.2	420	2	AAR97595	Aar97595	Adenoviru
363	30	73.2	421	2	AAR97598	Aar97598	Adenoviru
364	30	73.2	421	2	AAR97600	Aar97600	Adenoviru
365	30	73.2	421	2	AAR97601	Aar97601	Adenoviru
366	30	73.2	442	8	ADY08158	Ady08158	Plant ful
367	30	73.2	449	6	ABU18372	Abu18372	Protein e
368	30	73.2	449	8	ADR66318	Adr66318	Human pro
369	30	73.2	449	8	ADR66660	Adr66660	Human pro
370	30	73.2	452	4	ABG03526	Abg03526	Novel hum
371	30	73.2	456	9	ADV67457	Adv67457	Amino aci
372	30	73.2	477	8	ADN26088	Adn26088	Bacterial
373	30	73.2	480	8	ADR46683	Adr46683	Cancer-as
374	30	73.2	488	2	AAW02271	Aaw02271	Human pro
375	30	73.2	488	4	ABB56384	Abb56384	Non-endog
376	30	73.2	488	6	ABP81905	Abp81905	Human pro
377	30	73.2	488	6	AAO30984	Aao30984	Human pro
378	30	73.2	488	7	ADN40008	Adn40008	Cancer/an
379	30	73.2	488	8	ADO29622	Ado29622	Human GPC
380	30	73.2	488	8	ADR14169	Adr14169	Human NF-
381	30	73.2	488	8	ADR29413	Adr29413	Human G-p
382	30	73.2	488	9	ADW42777	Adw42777	Prostagla
383	30	73.2	488	9	ADY19546	Ady19546	PRO polyp
384	30	73.2	488	9	ADY15438	Ady15438	PRO polyp
385	30	73.2	488	9	ADZ64862	Adz64862	Human pro
386	30	73.2	489	3	AAY84603	Aay84603	Amino aci
387	30	73.2	490	4	ABG26292	Abg26292	Novel hum
388	30	73.2	490	6	ABR57071	Abr57071	Baboon/ma
389	30	73.2	490	7	ADH11546	Adh11546	Chimpanze
390	30	73.2	513	2	AAR42282	Aar42282	PGE2 rece
391	30	73.2	513	8	ADO29623	Ado29623	Mouse GPC
392	30	73.2	515	8	ADY12487	Ady12487	Plant ful
393	30	73.2	518	4	ABG04092	Abg04092	Novel hum
394	30	73.2	532	7	ADB67810	Adb67810	Human lun
395	30	73.2	586	8	ADN48236	Adn48236	Thermococ
396	30	73.2	604	5	ABP65574	Abp65574	Bifidobac
397	30	73.2	634	8	ABO84900	Abo84900	Human can
398	30	73.2	638	6	ABU36072	Abu36072	Protein e
399	30	73.2	641	4	ABG22668	Abg22668	Novel hum
400	30	73.2	666	7	ADH88274	Adh88274	Enterococ
401	30	73.2	681	6	ABU36220	Abu36220	Protein e
402	30	73.2	690	5	ABP53682	Abp53682	Human myo
403	30	73.2	724	8	ABO84902	Abo84902	Human can
404	30	73.2	745	8	ABO84899	Abo84899	Murine ca
405	30	73.2	758	4	ABG08865	Abg08865	Novel hum
406	30	73.2	780	8	ADI82549	Adi82549	Human mod
407	30	73.2	814	5	ABP35632	Abp35632	Fungal ZB

408	30	73.2	815	3	AAy54134	Aay54134	Amino aci
409	30	73.2	821	2	AAR35451	Aar35451	Mouse eps
410	30	73.2	821	5	ADZ58705	Adz58705	Mouse EPS
411	30	73.2	822	8	ADH09483	Adh09483	Human hos
412	30	73.2	823	5	ABP65373	Abp65373	Bifidobac
413	30	73.2	825	8	ADH09485	Adh09485	Human hos
414	30	73.2	825	8	ADH09484	Adh09484	Human hos
415	30	73.2	825	8	ADH09486	Adh09486	Human hos
416	30	73.2	825	8	ADJ75527	Adj75527	Marker ge
417	30	73.2	829	5	ABG61897	Abg61897	Prostate
418	30	73.2	829	5	ABB81476	Abb81476	Human P-c
419	30	73.2	829	5	ABP54683	Abp54683	Metastati
420	30	73.2	829	5	ABJ05598	Abj05598	Breast ca
421	30	73.2	829	5	AAU97492	Aau97492	Human P-c
422	30	73.2	829	5	AAM50864	Aam50864	Cadherin
423	30	73.2	829	6	ABR58670	Abr58670	Human can
424	30	73.2	829	6	ABU56670	Abu56670	Lung canc
425	30	73.2	829	6	ABU56434	Abu56434	Lung canc
426	30	73.2	829	6	ABP58357	Abp58357	Human P-c
427	30	73.2	829	7	ADC15497	Adc15497	Human bas
428	30	73.2	829	7	ADD14190	Add14190	Human src
429	30	73.2	829	7	ADN39020	Adn39020	Cancer/an
430	30	73.2	829	7	ADN39482	Adn39482	Cancer/an
431	30	73.2	829	7	ADN39578	Adn39578	Cancer/an
432	30	73.2	829	7	ADN39928	Adn39928	Cancer/an
433	30	73.2	829	7	ADN39545	Adn39545	Cancer/an
434	30	73.2	829	7	ADN39465	Adn39465	Cancer/an
435	30	73.2	829	8	ADL06565	Adl06565	Human tum
436	30	73.2	829	8	ADL70229	Adl70229	Colon can
437	30	73.2	829	8	ADN59621	Adn59621	Colon neo
438	30	73.2	829	8	ADN03948	Adn03948	Antipsori
439	30	73.2	829	8	ADO28657	Ado28657	Human CAD
440	30	73.2	829	8	ADQ20015	Adq20015	Human sof
441	30	73.2	829	8	ADP26905	Adp26905	Human P-c
442	30	73.2	829	9	ADV73198	Adv73198	Human col
443	30	73.2	829	9	ADX83229	Adx83229	Human TEG
444	30	73.2	829	9	AEB87752	Aeb87752	Human P-c
445	30	73.2	845	8	ADR09802	Adr09802	Human pro
446	30	73.2	869	6	ABP59932	Abp59932	Microbial
447	30	73.2	889	8	ADX73703	Adx73703	Plant ful
448	30	73.2	904	7	ABO70511	Abo70511	Pseudomon
449	30	73.2	945	9	AEB47195	Aeb47195	Chimpanze
450	30	73.2	946	8	ADN24151	Adn24151	Bacterial
451	30	73.2	947	3	AAy68672	Aay68672	Amino aci
452	30	73.2	947	7	ADE08525	Ade08525	Novel pro
453	30	73.2	947	8	ADY06912	Ady06912	Plant ful
454	30	73.2	951	9	AEB47199	Aeb47199	Chimpanze
455	30	73.2	952	3	AAy68673	Aay68673	Amino aci
456	30	73.2	954	9	AEB47187	Aeb47187	Chimpanze
457	30	73.2	958	3	AAy68671	Aay68671	Amino aci
458	30	73.2	981	4	ABG21856	Abg21856	Novel hum
459	30	73.2	1007	5	ABB91898	Abb91898	Herbicida
460	30	73.2	1020	5	ABB97958	Abb97958	Human pro
461	30	73.2	1020	7	ADC30995	Adc30995	Human nov
462	30	73.2	1189	8	ADY09354	Ady09354	Plant ful
463	30	73.2	1218	9	AEB91413	Aeb91413	Microbial
464	30	73.2	1978	2	AAy07032	Aay07032	Breast ca

465	30	73.2	1978	6	ABR64250	Abr64250	Angiogene
466	30	73.2	1978	9	AEA52606	Aea52606	Human NP2
467	29	70.7	18	2	AAW66397	Aaw66397	Cationic
468	29	70.7	18	3	AAV91696	Aay91696	Cationic
469	29	70.7	18	6	ABU59573	Abu59573	Cationic
470	29	70.7	18	9	ADY67442	Ady67442	Tumor cel
471	29	70.7	23	7	ADC36151	Adc36151	Weed cont
472	29	70.7	29	4	AAM20800	Aam20800	Peptide #
473	29	70.7	29	4	ABB42383	Abb42383	Peptide #
474	29	70.7	29	4	AAM36192	Aam36192	Peptide #
475	29	70.7	29	4	ABB25853	Abb25853	Protein #
476	29	70.7	29	4	AAM76083	Aam76083	Human bon
477	29	70.7	29	4	AAM63271	Aam63271	Human bra
478	29	70.7	29	4	ABG57807	Abg57807	Human liv
479	29	70.7	29	5	ABG45465	Abg45465	Human pep
480	29	70.7	48	5	ABG44107	Abg44107	Human pep
481	29	70.7	59	4	AAM88038	Aam88038	Human imm
482	29	70.7	66	8	ADL27373	Adl27373	Amino aci
483	29	70.7	83	5	ABP63696	Abp63696	Human ORF
484	29	70.7	86	5	AAE21585	Aae21585	Human gen
485	29	70.7	86	5	ABG65178	Abg65178	Human alb
486	29	70.7	86	6	ADA57248	Ada57248	Human sec
487	29	70.7	86	6	ADA41131	Ada41131	Human sec
488	29	70.7	86	6	ABR47937	Abr47937	Human sec
489	29	70.7	86	8	ADL78445	Adl78445	Albumin f
490	29	70.7	95	4	AAG74754	Aag74754	Human col
491	29	70.7	102	4	AAU41514	Aau41514	Propionib
492	29	70.7	102	4	AAU87112	Aau87112	Novel cen
493	29	70.7	102	4	ADM19915	Adm19915	Protein e
494	29	70.7	102	6	ABM38033	Abm38033	Propionib
495	29	70.7	102	8	ADI54427	Adi54427	Novel hum
496	29	70.7	108	4	AAG73514	Aag73514	Human col
497	29	70.7	110	4	AAO12578	Aao12578	Human pol
498	29	70.7	120	4	AAO00164	Aao00164	Human pol
499	29	70.7	124	6	ABP81211	Abp81211	Arabidops
500	29	70.7	140	4	AAO05812	Aao05812	Human pol
501	29	70.7	146	3	AAB41877	Aab41877	Human ORF
502	29	70.7	148	4	AAU52418	Aau52418	Propionib
503	29	70.7	148	6	ABM48937	Abm48937	Propionib
504	29	70.7	153	6	ABJ25830	Abj25830	Aspergill
505	29	70.7	154	4	AAM14784	Aam14784	Peptide #
506	29	70.7	154	4	ABB33751	Abb33751	Peptide #
507	29	70.7	154	4	AAM27209	Aam27209	Peptide #
508	29	70.7	154	4	ABB28566	Abb28566	Peptide #
509	29	70.7	154	4	ABB19195	Abb19195	Protein #
510	29	70.7	154	4	AAM66922	Aam66922	Human bon
511	29	70.7	154	4	AAM54518	Aam54518	Human bra
512	29	70.7	154	4	ABG48588	Abg48588	Human liv
513	29	70.7	154	4	AAM02507	Aam02507	Peptide #
514	29	70.7	154	5	ABG36581	Abg36581	Human pep
515	29	70.7	154	9	ADY66696	Ady66696	S. manson
516	29	70.7	167	6	ABJ26430	Abj26430	Aspergill
517	29	70.7	178	4	AAU29522	Aau29522	Novel hum
518	29	70.7	179	6	ADB06452	Adb06452	Alloiococ
519	29	70.7	182	8	ADX79705	Adx79705	Plant ful
520	29	70.7	182	8	ADY11580	Ady11580	Plant ful
521	29	70.7	182	8	ADX75533	Adx75533	Plant ful

522	29	70.7	182	8	ADY10451	Ady10451	Plant ful
523	29	70.7	188	4	ABG00123	Abg00123	Novel hum
524	29	70.7	190	4	ABB70193	Abb70193	Drosophil
525	29	70.7	190	8	ADR58985	Adr58985	Human Elk
526	29	70.7	200	5	ABP66332	Abp66332	Bifidobac
527	29	70.7	214	4	ABB65814	Abb65814	Drosophil
528	29	70.7	216	4	ABG00688	Abg00688	Novel hum
529	29	70.7	221	7	ADF04034	Adf04034	Bacterial
530	29	70.7	225	4	ABG14376	Abg14376	Novel hum
531	29	70.7	227	6	ADA35159	Ada35159	Acinetoba
532	29	70.7	230	6	ABM70652	Abm70652	Photorhab
533	29	70.7	232	8	ADX76865	Adx76865	Plant ful
534	29	70.7	236	4	ABB62200	Abb62200	Drosophil
535	29	70.7	251	3	AAB16536	Aab16536	Bacteriop
536	29	70.7	253	8	ADR86138	Adr86138	Aspergill
537	29	70.7	254	5	ABG97865	Abg97865	Negative-
538	29	70.7	254	5	ABG97850	Abg97850	Negative-
539	29	70.7	254	7	ADF68687	Adf68687	Human met
540	29	70.7	254	7	ADF68688	Adf68688	Human met
541	29	70.7	254	7	ADF89260	Adf89260	M protein
542	29	70.7	254	7	ADF89261	Adf89261	M protein
543	29	70.7	254	8	ADJ97148	Adj97148	M protein
544	29	70.7	254	8	ADJ97149	Adj97149	M protein
545	29	70.7	254	8	ADL07799	Adl07799	M protein
546	29	70.7	254	8	ADL07800	Adl07800	M protein
547	29	70.7	254	8	ADM67619	Adm67619	Human met
548	29	70.7	254	8	ADM67620	Adm67620	Human met
549	29	70.7	254	8	ADU26120	Adu26120	Human met
550	29	70.7	254	8	ADU26121	Adu26121	Human met
551	29	70.7	254	9	ADY84193	Ady84193	M protein
552	29	70.7	254	9	ADY84192	Ady84192	M protein
553	29	70.7	262	8	ADS15085	Ads15085	Pseudomon
554	29	70.7	268	7	ABO82052	Abo82052	Pseudomon
555	29	70.7	272	6	ABU22646	Abu22646	Protein e
556	29	70.7	273	6	ABU19716	Abu19716	Protein e
557	29	70.7	280	8	ADM97722	Adm97722	Human MNA
558	29	70.7	281	6	AAE35493	Aae35493	Streptomy
559	29	70.7	288	8	ADI62525	Adi62525	Mouse LRH
560	29	70.7	288	8	ADY22635	Ady22635	Plant ful
561	29	70.7	293	4	ABG09309	Abg09309	Novel hum
562	29	70.7	296	4	ABB65345	Abb65345	Drosophil
563	29	70.7	303	6	ABU21346	Abu21346	Protein e
564	29	70.7	314	8	ADP45414	Adp45414	Human col
565	29	70.7	316	8	ADP45413	Adp45413	Human col
566	29	70.7	320	8	ADS30059	Ads30059	Bacterial
567	29	70.7	338	8	ADT60373	Adt60373	Plant pol
568	29	70.7	344	8	ADS24368	Ads24368	Bacterial
569	29	70.7	349	4	ABB63062	Abb63062	Drosophil
570	29	70.7	359	8	ADN21165	Adn21165	Bacterial
571	29	70.7	383	9	ABM90916	Abm90916	M. xanthu
572	29	70.7	392	8	ADP45412	Adp45412	Human col
573	29	70.7	392	8	ADT07548	Adt07548	Human col
574	29	70.7	397	5	ABP35601	Abp35601	Fungal ZB
575	29	70.7	408	7	ADC36134	Adc36134	Weed cont
576	29	70.7	418	6	ADA36357	Ada36357	Acinetoba
577	29	70.7	421	8	ADT60948	Adt60948	Plant pol
578	29	70.7	424	8	ADS78293	Ads78293	Aminotran

579	29	70.7	425	7	ABO77094	Abo77094	Pseudomon
580	29	70.7	426	5	ABB92936	Abb92936	Herbicida
581	29	70.7	428	3	AAG49998	Aag49998	Arabidops
582	29	70.7	428	3	AAG06332	Aag06332	Arabidops
583	29	70.7	440	5	ABP47766	Abp47766	Protein #
584	29	70.7	440	5	ABP47767	Abp47767	Protein #
585	29	70.7	440	5	ABP47765	Abp47765	Protein #
586	29	70.7	441	8	ADX68020	Adx68020	Plant ful
587	29	70.7	445	9	ADX83076	Adx83076	DNA encod
588	29	70.7	449	5	ABJ05512	Abj05512	Human bre
589	29	70.7	449	6	ABP96644	Abp96644	Mouse G3B
590	29	70.7	449	6	ABJ19760	Abj19760	Human MP2
591	29	70.7	454	3	AAG06059	Aag06059	Arabidops
592	29	70.7	456	3	AAG39609	Aag39609	Arabidops
593	29	70.7	460	6	ABU22409	Abu22409	Protein e
594	29	70.7	467	6	ABU34965	Abu34965	Protein e
595	29	70.7	469	8	ADM97707	Adm97707	Human MNA
596	29	70.7	469	8	ADM97717	Adm97717	Human MNA
597	29	70.7	469	8	ADM97718	Adm97718	Human MNA
598	29	70.7	469	8	ADM97716	Adm97716	Human MNA
599	29	70.7	473	8	ADN21795	Adn21795	Bacterial
600	29	70.7	478	4	AAU23663	Aau23663	Novel hum
601	29	70.7	482	6	ABP96642	Abp96642	Mouse G3B
602	29	70.7	482	6	ABP96641	Abp96641	Human G3B
603	29	70.7	482	7	ADE60267	Ade60267	Human Pro
604	29	70.7	482	7	ADE59955	Ade59955	Human Pro
605	29	70.7	482	7	ADE59946	Ade59946	Human Pro
606	29	70.7	482	7	ADE59949	Ade59949	Human Pro
607	29	70.7	482	7	ADE59952	Ade59952	Human Pro
608	29	70.7	482	8	ADH51303	Adh51303	Ras-GTPas
609	29	70.7	482	8	ADP45411	Adp45411	Human col
610	29	70.7	482	8	ADT07547	Adt07547	Human col
611	29	70.7	482	9	ADW08693	Adw08693	Human pro
612	29	70.7	483	8	ADN24554	Adn24554	Bacterial
613	29	70.7	490	4	AAU23108	Aau23108	Novel hum
614	29	70.7	491	7	ABO65717	Abo65717	Klebsiell
615	29	70.7	495	8	ADM97725	Adm97725	Human MNA
616	29	70.7	504	4	ABB66372	Abb66372	Drosophil
617	29	70.7	513	6	ABU41585	Abu41585	Protein e
618	29	70.7	515	8	ADM97724	Adm97724	MNAR prot
619	29	70.7	522	3	AAG06331	Aag06331	Arabidops
620	29	70.7	522	3	AAG49997	Aag49997	Arabidops
621	29	70.7	525	3	AAG49996	Aag49996	Arabidops
622	29	70.7	526	3	AAG06330	Aag06330	Arabidops
623	29	70.7	530	8	ADT56334	Adt56334	Plant pol
624	29	70.7	533	4	ABB60779	Abb60779	Drosophil
625	29	70.7	542	4	ABB66844	Abb66844	Drosophil
626	29	70.7	544	9	AEB44550	Aeb44550	Sleep dis
627	29	70.7	548	3	AAG06058	Aag06058	Arabidops
628	29	70.7	550	3	AAG39608	Aag39608	Arabidops
629	29	70.7	558	3	AAG06057	Aag06057	Arabidops
630	29	70.7	560	2	AAY21814	Aay21814	Mouse liv
631	29	70.7	560	3	AAG39607	Aag39607	Arabidops
632	29	70.7	560	8	ADI62533	Adi62533	Mouse LRH
633	29	70.7	560	8	ADP05715	Adp05715	Mouse nuc
634	29	70.7	568	2	AAW19395	Aaw19395	Human cal
635	29	70.7	568	7	ADD13117	Add13117	Human TSB

636	29	70.7	568	8	ADS22574	Ads22574	Bacterial
637	29	70.7	568	9	ADY91710	Ady91710	Human c6o
638	29	70.7	573	4	AAU35664	Aau35664	Haemophil
639	29	70.7	573	6	ABU30625	Abu30625	Protein e
640	29	70.7	584	8	ADS26179	Ads26179	Bacterial
641	29	70.7	590	8	ADS25699	Ads25699	Bacterial
642	29	70.7	598	4	ABB58590	Abb58590	Drosophil
643	29	70.7	602	5	AAU93023	Aau93023	Arabidops
644	29	70.7	602	7	ADD30514	Add30514	Plant yie
645	29	70.7	602	8	ADI43937	Adi43937	Plant tra
646	29	70.7	602	8	ADI61403	Adi61403	A. thalia
647	29	70.7	602	8	ADT55609	Adt55609	Plant pol
648	29	70.7	608	4	ABB64278	Abb64278	Drosophil
649	29	70.7	629	8	ADI26782	Adi26782	Schizosac
650	29	70.7	638	8	ADQ96030	Adq96030	T cell ac
651	29	70.7	638	8	ADQ96032	Adq96032	T cell ac
652	29	70.7	660	9	ABM95169	Abm95169	M. xanthu
653	29	70.7	681	8	ADO51708	Ado51708	Streptomy
654	29	70.7	684	6	ABM67159	Abm67159	Photorhab
655	29	70.7	697	8	ADU07653	Adu07653	Amino aci
656	29	70.7	709	8	ADR13753	Adr13753	Amidase,
657	29	70.7	739	4	ABG25754	Abg25754	Novel hum
658	29	70.7	742	8	ADS44217	Ads44217	Bacterial
659	29	70.7	759	8	ADX91651	Adx91651	Plant ful
660	29	70.7	761	7	ADF74131	Adf74131	Human nov
661	29	70.7	798	6	ABU17132	Abu17132	Protein e
662	29	70.7	805	4	ABB66534	Abb66534	Drosophil
663	29	70.7	807	3	AAB18311	Aab18311	Plasmodiu
664	29	70.7	807	7	ABO23607	Abo23607	Plasmodiu
665	29	70.7	814	6	ADA33086	Ada33086	Acinetoba
666	29	70.7	824	4	AAB93025	Aab93025	Human pro
667	29	70.7	824	7	ADM39521	Adm39521	Human Gem
668	29	70.7	824	9	ADZ85655	Adz85655	Human gem
669	29	70.7	833	6	ABP78673	Abp78673	N. gonorr
670	29	70.7	837	5	ABJ10804	Abj10804	Rabbit HC
671	29	70.7	872	7	ADE08380	Ade08380	Novel pro
672	29	70.7	873	4	AAM93552	Aam93552	Human pol
673	29	70.7	873	8	ADL31282	Adl31282	Human pro
674	29	70.7	875	8	ADS28775	Ads28775	Bacterial
675	29	70.7	880	9	ADX83085	Adx83085	Human PEL
676	29	70.7	881	4	ABG01472	Abg01472	Novel hum
677	29	70.7	895	4	ABB63419	Abb63419	Drosophil
678	29	70.7	905	2	AAW31186	Aaw31186	Human p16
679	29	70.7	925	8	ADM97706	Adm97706	Murine MN
680	29	70.7	938	5	ABP69053	Abp69053	Human pol
681	29	70.7	970	5	ABP65559	Abp65559	Bifidobac
682	29	70.7	983	8	ADM87342	Adm87342	Human pro
683	29	70.7	985	4	ABB63557	Abb63557	Drosophil
684	29	70.7	985	4	ABB66752	Abb66752	Drosophil
685	29	70.7	1021	7	ADJ68507	Adj68507	Human hea
686	29	70.7	1029	8	ADI26790	Adi26790	Saccharom
687	29	70.7	1096	3	AAB43253	Aab43253	Human ORF
688	29	70.7	1097	4	ABG02027	Abg02027	Novel hum
689	29	70.7	1130	7	ADC99065	Adc99065	Human KPP
690	29	70.7	1130	8	ADM97695	Adm97695	Human MNA
691	29	70.7	1130	8	ABM81812	Abm81812	Tumour-as
692	29	70.7	1130	9	ADX83072	Adx83072	Proline,

693	29	70.7	1135	2	AAW31185	Aaw31185	Human	p16
694	29	70.7	1248	4	ABG19706	Abg19706	Novel	hum
695	29	70.7	1251	7	ADE09332	Ade09332	Novel	pro
696	29	70.7	1251	8	ADM87788	Adm87788	Human	EST
697	29	70.7	1269	4	ABB65201	Abb65201	Drosophil	
698	29	70.7	1278	4	ABB71882	Abb71882	Drosophil	
699	29	70.7	1278	6	ABG74682	Abg74682	Human	CGD
700	29	70.7	1278	8	ADS96466	Ads96466	Drosophil	
701	29	70.7	1313	6	ABU48939	Abu48939	Protein	e
702	29	70.7	1345	5	AAE25097	Aae25097	Human	kin
703	29	70.7	1353	7	ADA27376	Ada27376	Human	CAP
704	29	70.7	1353	8	ADS10793	Ads10793	Human	the
705	29	70.7	1390	5	ABG96292	Abg96292	Human	ova
706	29	70.7	1390	8	ADQ19160	Adq19160	Human	sof
707	29	70.7	1454	7	ADJ69522	Adj69522	Human	hea
708	29	70.7	1460	4	ABB71977	Abb71977	Drosophil	
709	29	70.7	1464	2	AAW79294	Aaw79294	An	antige
710	29	70.7	1486	5	ABG97854	Abg97854	Negative-	
711	29	70.7	1493	6	ABU03484	Abu03484	Angiogene	
712	29	70.7	1498	6	ABP98844	Abp98844	Human	str
713	29	70.7	1553	8	ADQ96036	Adq96036	T cell	ac
714	29	70.7	1616	6	ABU35669	Abu35669	Protein	e
715	29	70.7	1616	7	ABO23515	Abo23515	Mycoplasma	
716	29	70.7	1751	9	ADV97877	Adv97877	Murine	pr
717	29	70.7	1806	8	ADU05710	Adu05710	Cellulose	
718	29	70.7	1835	9	ADW07654	Adw07654	Human	MPT
719	29	70.7	2073	8	ADQ26424	Adq26424	Schizosac	
720	29	70.7	2073	8	ADR88319	Adr88319	Schizosac	
721	29	70.7	2091	8	ADN61449	Adn61449	Human	KPP
722	29	70.7	2132	9	ADV97875	Adv97875	Murine	pr
723	29	70.7	2141	5	ABB81196	Abb81196	Human	PN1
724	29	70.7	2141	9	ADZ97856	Adz97856	Human	PN1
725	29	70.7	2193	6	ABR42219	Abr42219	Human	pro
726	29	70.7	2217	9	ADX98203	Adx98203	Lysine	de
727	29	70.7	2219	8	ADN00364	Adn00364	Novel	hum
728	29	70.7	2245	8	ADJ96651	Adj96651	Human	Nim
729	29	70.7	2289	2	AAW14987	Aaw14987	Protein	d
730	29	70.7	2376	6	ABR58313	Abr58313	BCU0586	p
731	29	70.7	2376	8	ADQ96034	Adq96034	T cell	ac
732	29	70.7	2659	4	ABB68426	Abb68426	Drosophil	
733	29	70.7	4019	4	AAE13839	Aae13839	Human	lun
734	29	70.7	4019	7	ADD66733	Add66733	Human	lun
735	29	70.7	4019	7	ADE87987	Ade87987	Human	lun
736	29	70.7	4025	5	ABP69736	Abp69736	Human	pol
737	29	70.7	4025	8	ADU18074	Adu18074	Human	can
738	29	70.7	4773	7	ADJ95094	Adj95094	Novel	NOV
739	29	70.7	7349	6	ABU11385	Abu11385	Protein	e
740	29	70.7	8360	6	AAE35499	Aae35499	Streptomy	
741	28	68.3	20	2	AAW36611	Aaw36611	Human	E-C
742	28	68.3	20	3	AAY54887	Aay54887	Fragment	
743	28	68.3	50	8	ADU69732	Adu69732	S	agalact
744	28	68.3	54	3	AAG19837	Aag19837	Arabidops	
745	28	68.3	56	5	ABP32376	Abp32376	Human	ORF
746	28	68.3	60	4	AAU41784	Aau41784	Propionib	
747	28	68.3	60	6	ABM38303	Abm38303	Propionib	
748	28	68.3	61	4	AAU60201	Aau60201	Propionib	
749	28	68.3	61	6	ABM56720	Abm56720	Propionib	

750	28	68.3	71	4	AAM85662	Aam85662	Human imm
751	28	68.3	72	5	ABP32838	Abp32838	Human ORF
752	28	68.3	77	8	ADX87418	Adx87418	Plant ful
753	28	68.3	83	4	ABG00200	Abg00200	Novel hum
754	28	68.3	86	3	AAG19836	Aag19836	Arabidops
755	28	68.3	89	4	AAU55664	Aau55664	Propionib
756	28	68.3	89	6	ABM52183	Abm52183	Propionib
757	28	68.3	90	4	AAO10784	Aao10784	Human pol
758	28	68.3	95	3	AAB58533	Aab58533	Lung canc
759	28	68.3	95	5	ABG77076	Abg77076	Prostate
760	28	68.3	98	5	ABG59992	Abg59992	Human DIT
761	28	68.3	103	4	AAU58140	Aau58140	Propionib
762	28	68.3	103	6	ABM54659	Abm54659	Propionib
763	28	68.3	104	3	AAG43260	Aag43260	Arabidops
764	28	68.3	109	3	AAG54907	Aag54907	Arabidops
765	28	68.3	115	4	ABG20378	Abg20378	Novel hum
766	28	68.3	118	4	AAO06839	Aao06839	Human pol
767	28	68.3	119	5	ADK36907	Adk36907	Novel hum
768	28	68.3	120	4	ABG08728	Abg08728	Novel hum
769	28	68.3	122	4	AAO06483	Aao06483	Human pol
770	28	68.3	124	5	ABU50986	Abu50986	Helicobac
771	28	68.3	126	3	AAB41464	Aab41464	Human ORF
772	28	68.3	126	5	ABP34285	Abp34285	Human ORF
773	28	68.3	126	7	ADM05810	Adm05810	Human pro
774	28	68.3	131	4	ABB69234	Abb69234	Drosophil
775	28	68.3	131	4	AAO02911	Aao02911	Human pol
776	28	68.3	136	3	AAG43259	Aag43259	Arabidops
777	28	68.3	139	7	ADF30320	Adf30320	Human can
778	28	68.3	139	7	ABO69462	Abo69462	Pseudomon
779	28	68.3	141	4	ABG04850	Abg04850	Novel hum
780	28	68.3	142	3	AAG26489	Aag26489	Arabidops
781	28	68.3	143	3	AAY54054	Aay54054	Angiostat
782	28	68.3	144	5	ABG59986	Abg59986	Human DIT
783	28	68.3	146	3	AAG26488	Aag26488	Arabidops
784	28	68.3	148	6	ABR40796	Abr40796	Oryza sat
785	28	68.3	148	6	ABR40665	Abr40665	Oryza sat
786	28	68.3	149	4	ABG17169	Abg17169	Novel hum
787	28	68.3	151	8	ADT50935	Adt50935	Cancer re
788	28	68.3	152	3	AAG54787	Aag54787	Arabidops
789	28	68.3	152	4	AAU48347	Aau48347	Propionib
790	28	68.3	152	6	ABM44866	Abm44866	Propionib
791	28	68.3	158	7	ABM88068	Abm88068	Rice abio
792	28	68.3	159	6	ABU36976	Abu36976	Protein e
793	28	68.3	159	8	ABO60059	Abo60059	Human gen
794	28	68.3	159	8	ADO19083	Ado19083	Human PRO
795	28	68.3	160	2	AAR92703	Aar92703	Pea HY4 g
796	28	68.3	161	3	AAG26487	Aag26487	Arabidops
797	28	68.3	161	7	ADC01631	Adc01631	Enteroha
798	28	68.3	164	6	ABM65448	Abm65448	Propionib
799	28	68.3	167	2	AAW64467	Aaw64467	Human sec
800	28	68.3	167	4	AAB90742	Aab90742	Human CR6
801	28	68.3	169	7	ABO72836	Abo72836	Pseudomon
802	28	68.3	171	3	AAB40484	Aab40484	Human ORF
803	28	68.3	171	5	ABP06779	Abp06779	Human ORF
804	28	68.3	178	4	AAB63845	Aab63845	Human pro
805	28	68.3	181	7	ABM89895	Abm89895	Rice abio
806	28	68.3	182	3	AAB11648	Aab11648	A. vitis

807	28	68.3	191	4	ABB63745	Abb63745	Drosophil
808	28	68.3	203	5	ABG60116	Abg60116	Human DIT
809	28	68.3	206	5	AAE20841	Aae20841	Human gen
810	28	68.3	207	6	ADB12511	Adb12511	Alloiococ
811	28	68.3	214	7	ADE31080	Ade31080	Human dia
812	28	68.3	216	7	ABO74722	Abo74722	Pseudomon
813	28	68.3	225	8	ADY23757	Ady23757	Plant ful
814	28	68.3	228	8	ADY22772	Ady22772	Plant ful
815	28	68.3	229	8	ADT56948	Adt56948	Plant pol
816	28	68.3	237	8	ADN97346	Adn97346	Murine NK
817	28	68.3	240	9	AEA63761	Aea63761	Methionin
818	28	68.3	243	6	ADA35771	Ada35771	Acinetoba
819	28	68.3	244	5	ABP08045	Abp08045	Human ORF
820	28	68.3	244	8	ADX78996	Adx78996	Plant ful
821	28	68.3	248	6	ABU11817	Abu11817	Human MDD
822	28	68.3	252	6	ABM68267	Abm68267	Photorhab
823	28	68.3	254	5	ABG97866	Abg97866	Negative-
824	28	68.3	254	7	ADF68689	Adf68689	Human met
825	28	68.3	254	7	ADF68690	Adf68690	Human met
826	28	68.3	254	7	ADF89262	Adf89262	M protein
827	28	68.3	254	7	ADF89263	Adf89263	M protein
828	28	68.3	254	8	ADJ97150	Adj97150	M protein
829	28	68.3	254	8	ADJ97151	Adj97151	M protein
830	28	68.3	254	8	ADL07802	Adl07802	M protein
831	28	68.3	254	8	ADL07801	Adl07801	M protein
832	28	68.3	254	8	ADM67621	Adm67621	Human met
833	28	68.3	254	8	ADM67622	Adm67622	Human met
834	28	68.3	254	8	ADU26122	Adu26122	Human met
835	28	68.3	254	8	ADU26123	Adu26123	Human met
836	28	68.3	254	9	ADY84195	Ady84195	M protein
837	28	68.3	254	9	ADY84194	Ady84194	M protein
838	28	68.3	255	9	AEA63758	Aea63758	Methionin
839	28	68.3	260	8	ADX76192	Adx76192	Plant ful
840	28	68.3	261	3	AAG06181	Aag06181	Arabidops
841	28	68.3	265	3	AAG06180	Aag06180	Arabidops
842	28	68.3	265	8	ADJ63826	Adj63826	Plant lip
843	28	68.3	265	8	ADX88760	Adx88760	Plant ful
844	28	68.3	268	4	AAB92568	Aab92568	Human pro
845	28	68.3	269	4	ABG20379	Abg20379	Novel hum
846	28	68.3	273	8	ADO02598	Ado02598	Thalecres
847	28	68.3	273	8	ADO62233	Ado62233	Transcrip
848	28	68.3	275	7	ABR57185	Abr57185	Human EDT
849	28	68.3	276	8	ADS26657	Ads26657	Bacterial
850	28	68.3	276	8	ADS27049	Ads27049	Bacterial
851	28	68.3	279	4	AAB63844	Aab63844	Human pro
852	28	68.3	281	3	AAG06179	Aag06179	Arabidops
853	28	68.3	288	4	AAM42286	Aam42286	Human bre
854	28	68.3	288	4	AAM96245	Aam96245	Human rep
855	28	68.3	291	8	ADS42040	Ads42040	Bacterial
856	28	68.3	292	5	ABU52263	Abu52263	Helicobac
857	28	68.3	294	8	ABM81436	Abm81436	Tumour-as
858	28	68.3	294	8	ADS26291	Ads26291	Bacterial
859	28	68.3	302	8	ADQ67686	Adq67686	Novel hum
860	28	68.3	302	8	ADR10278	Adr10278	Human pro
861	28	68.3	307	3	AAG06541	Aag06541	Arabidops
862	28	68.3	309	9	ABM92047	Abm92047	M. xanthu
863	28	68.3	315	5	ABB49189	Abb49189	Listeria

864	28	68.3	329	8	ADQ66325	Adq66325	Novel hum
865	28	68.3	330	5	ABP65683	Abp65683	Bifidobac
866	28	68.3	333	8	ADY04511	Ady04511	Plant ful
867	28	68.3	333	9	ABM91340	Abm91340	M. xanthu
868	28	68.3	334	4	ABG18622	Abg18622	Novel hum
869	28	68.3	336	3	AAB53152	Aab53152	Macaca mu
870	28	68.3	338	8	ADT59586	Adt59586	Plant pol
871	28	68.3	340	8	ADX79760	Adx79760	Plant ful
872	28	68.3	342	8	ADP98832	Adp98832	C. albica
873	28	68.3	344	4	ABG02457	Abg02457	Novel hum
874	28	68.3	346	8	ADX74326	Adx74326	Plant ful
875	28	68.3	347	8	ADN99770	Adn99770	Novel hum
876	28	68.3	349	6	ABU27671	Abu27671	Protein e
877	28	68.3	351	4	ABG08730	Abg08730	Novel hum
878	28	68.3	353	7	ADB63898	Adb63898	Human pro
879	28	68.3	355	3	AAY53884	Aay53884	A suppres
880	28	68.3	355	3	AAB57084	Aab57084	Human pro
881	28	68.3	355	8	ADX76365	Adx76365	Plant ful
882	28	68.3	355	8	ADX89045	Adx89045	Plant ful
883	28	68.3	362	4	ABG18548	Abg18548	Novel hum
884	28	68.3	364	8	ADH56301	Adh56301	L. escul
885	28	68.3	369	8	ADJ49689	Adj49689	Oil-assoc
886	28	68.3	369	8	ADX76372	Adx76372	Plant ful
887	28	68.3	374	2	AAR45939	Aar45939	A glycosy
888	28	68.3	374	2	AAW13642	Aaw13642	Human alp
889	28	68.3	374	8	ABG75491	Abg75491	Human alp
890	28	68.3	376	6	ABU34393	Abu34393	Protein e
891	28	68.3	377	7	ADH88337	Adh88337	Enterococ
892	28	68.3	388	4	AAG81145	Aag81145	Mycobacte
893	28	68.3	388	8	ADM16694	Adm16694	PRL-P4-G7
894	28	68.3	389	6	ABU36612	Abu36612	Protein e
895	28	68.3	389	8	ADX93736	Adx93736	Plant ful
896	28	68.3	391	3	AAG16883	Aag16883	Arabidops
897	28	68.3	391	6	ABU18760	Abu18760	Protein e
898	28	68.3	391	8	ADN27216	Adn27216	Bacterial
899	28	68.3	393	6	ABU17952	Abu17952	Protein e
900	28	68.3	393	6	ABU34083	Abu34083	Protein e
901	28	68.3	393	8	ADS27583	Ads27583	Bacterial
902	28	68.3	393	8	ADT60626	Adt60626	Plant pol
903	28	68.3	394	8	ADS29582	Ads29582	Bacterial
904	28	68.3	396	8	ADX90151	Adx90151	Plant ful
905	28	68.3	396	8	ADX96537	Adx96537	Plant ful
906	28	68.3	398	7	ADC36354	Adc36354	Weed cont
907	28	68.3	398	7	ADC36356	Adc36356	Weed cont
908	28	68.3	399	4	ABG08731	Abg08731	Novel hum
909	28	68.3	399	8	ADY13551	Ady13551	Plant ful
910	28	68.3	400	8	ADN26089	Adn26089	Bacterial
911	28	68.3	401	8	ADS22438	Ads22438	Bacterial
912	28	68.3	401	8	ADS25411	Ads25411	Bacterial
913	28	68.3	401	8	ADS25530	Ads25530	Bacterial
914	28	68.3	401	8	ADS26146	Ads26146	Bacterial
915	28	68.3	404	3	AAG26231	Aag26231	Arabidops
916	28	68.3	404	3	AAG42551	Aag42551	Arabidops
917	28	68.3	405	8	ADX74870	Adx74870	Plant ful
918	28	68.3	406	6	ABP95992	Abp95992	Streptomy
919	28	68.3	409	8	ADN21442	Adn21442	Bacterial
920	28	68.3	411	5	ADK34897	Adk34897	Novel hum

921	28	68.3	411	9	ABM95987	Abm95987	M. xanthu
922	28	68.3	412	5	ABP43924	Abp43924	FLJ10159
923	28	68.3	417	7	ABR57183	Abr57183	Human EDT
924	28	68.3	417	8	ABM80414	Abm80414	Tumour-as
925	28	68.3	418	8	ADS30176	Ads30176	Bacterial
926	28	68.3	421	8	ADN25167	Adn25167	Bacterial
927	28	68.3	426	3	AAG26230	Aag26230	Arabidops
928	28	68.3	426	3	AAG42550	Aag42550	Arabidops
929	28	68.3	426	8	ADX79999	Adx79999	Plant ful
930	28	68.3	427	7	ADH89321	Adh89321	G. max 7S
931	28	68.3	427	8	ADG44117	Adg44117	G. max se
932	28	68.3	428	8	ADN19902	Adn19902	Bacterial
933	28	68.3	429	4	ABG18605	Abg18605	Novel hum
934	28	68.3	429	6	ADA36746	Ada36746	Acinetoba
935	28	68.3	433	9	ADW18647	Adw18647	Eucalyptu
936	28	68.3	434	8	ADS44046	Ads44046	Bacterial
937	28	68.3	437	3	AAG26229	Aag26229	Arabidops
938	28	68.3	439	8	ADX72399	Adx72399	Plant ful
939	28	68.3	439	8	ADX74436	Adx74436	Plant ful
940	28	68.3	439	8	ADX74708	Adx74708	Plant ful
941	28	68.3	440	8	ADX89117	Adx89117	Plant ful
942	28	68.3	440	8	ADX76370	Adx76370	Plant ful
943	28	68.3	440	8	ADX76224	Adx76224	Plant ful
944	28	68.3	440	8	ADX77924	Adx77924	Plant ful
945	28	68.3	440	8	ADY24029	Ady24029	Plant ful
946	28	68.3	441	3	AAG42549	Aag42549	Arabidops
947	28	68.3	441	8	ADX76266	Adx76266	Plant ful
948	28	68.3	441	8	ADY24506	Ady24506	Plant ful
949	28	68.3	441	8	ADX89047	Adx89047	Plant ful
950	28	68.3	441	8	ADX75845	Adx75845	Plant ful
951	28	68.3	441	8	ADX89046	Adx89046	Plant ful
952	28	68.3	441	8	ADY24134	Ady24134	Plant ful
953	28	68.3	441	8	ADX88749	Adx88749	Plant ful
954	28	68.3	442	8	ADY24193	Ady24193	Plant ful
955	28	68.3	442	8	ADX74652	Adx74652	Plant ful
956	28	68.3	442	8	ADY24140	Ady24140	Plant ful
957	28	68.3	442	8	ADY24505	Ady24505	Plant ful
958	28	68.3	442	8	ADX90794	Adx90794	Plant ful
959	28	68.3	442	8	ADX73816	Adx73816	Plant ful
960	28	68.3	442	8	ADY24135	Ady24135	Plant ful
961	28	68.3	442	8	ADX75346	Adx75346	Plant ful
962	28	68.3	443	8	ADX87578	Adx87578	Plant ful
963	28	68.3	445	6	AAO27493	Aao27493	Garden ba
964	28	68.3	452	3	AAG27711	Aag27711	Arabidops
965	28	68.3	452	7	ADC99052	Adc99052	Human KPP
966	28	68.3	454	8	ADP20605	Adp20605	Infectiou
967	28	68.3	456	5	ABP68956	Abp68956	Human pol
968	28	68.3	457	4	AAU35592	Aau35592	Haemophil
969	28	68.3	457	6	ABU30494	Abu30494	Protein e
970	28	68.3	463	8	ADN96092	Adn96092	Human NOV
971	28	68.3	465	9	AEA22086	Aea22086	Campyloba
972	28	68.3	466	8	ADI40989	Adi40989	Guinea pi
973	28	68.3	468	5	ABP69176	Abp69176	Human pol
974	28	68.3	469	7	ADF55454	Adf55454	Human nov
975	28	68.3	469	8	ADN20369	Adn20369	Bacterial
976	28	68.3	470	4	ABG21932	Abg21932	Novel hum
977	28	68.3	471	5	ABB98169	Abb98169	Bovine tu

978	28	68.3	471	5	AAE25816	Aae25816	Bovine tu
979	28	68.3	471	7	ADD46086	Add46086	Rat Prote
980	28	68.3	471	7	ADD44724	Add44724	Human Pro
981	28	68.3	471	7	ADD44722	Add44722	Rat Prote
982	28	68.3	471	7	ADD46088	Add46088	Human Pro
983	28	68.3	471	8	ADS88298	Ads88298	Human pro
984	28	68.3	471	8	ADS88331	Ads88331	Human pro
985	28	68.3	473	6	ABU18753	Abu18753	Protein e
986	28	68.3	475	8	ADS42328	Ads42328	Bacterial
987	28	68.3	476	7	ADF28933	Adf28933	Sheep ang
988	28	68.3	476	9	AEA26771	Aea26771	Stress to
989	28	68.3	476	9	AEA27400	Aea27400	Stress to
990	28	68.3	479	5	ABP43965	Abp43965	Unidentif
991	28	68.3	479	7	ADD31031	Add31031	Plant yie
992	28	68.3	479	8	ADI44375	Adi44375	Plant tra
993	28	68.3	479	9	ADW26707	Adw26707	Fructo-ol
994	28	68.3	479	9	AEA26841	Aea26841	Stress to
995	28	68.3	481	5	ABB08866	Abb08866	Corynebac
996	28	68.3	481	8	ADS29747	Ads29747	Bacterial
997	28	68.3	482	5	AAE26856	Aae26856	Anabaena
998	28	68.3	483	8	ADN20080	Adn20080	Bacterial
999	28	68.3	490	5	ABP65478	Abp65478	Bifidobac
1000	28	68.3	492	8	ADN20518	Adn20518	Bacterial

ALIGNMENTS

RESULT 1

AAW64677

ID AAW64677 standard; protein; 8 AA.

XX

AC AAW64677;

XX

DT 04-NOV-1998 (first entry)

XX

DE Human ADNF-III peptide fragment.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;

KW activity dependent neuroprotective protein; neurone; excito-toxicity;

KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;

KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;

KW HIV infection.

XX

OS Homo sapiens.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.

XX

PA (USSH) US SEC HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Brenneman DE, Bassan M;

XX
 DR WPI; 1998-447239/38.
 XX
 PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excito-toxicity or Alzheimer's disease.
 XX
 PS Example 20; Page 75; 121pp; English.
 XX
 CC This sequence represents a peptide used in a method which isolates a
 CC novel activity dependent neurotrophic factor III, ADNF-III (also known as
 CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
 CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurones associated with
 CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
 CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 1 NAPVSIPQ 8

RESULT 2

AAW64678

ID AAW64678 standard; protein; 8 AA.

XX

AC AAW64678;

XX

DT 04-NOV-1998 (first entry)

XX

DE Human ADNF-III derived active peptide #2.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
 KW activity dependent neuroprotective protein; neurone; excito-toxicity;
 KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
 KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
 KW HIV infection.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal Asn is modified by the presence of an

FT (R1)x group where R1 is an amino acid sequence of 1 to 40

FT amino acids wherein each amino acid is independently

FT selected from a group consisting of naturally occurring

FT amino acids and amino acid mimetics"
 FT Modified-site 8
 FT /note= "C-terminal Gln is modified by the presence of an
 FT (R2)y group where R2 is an amino acid sequence of 1 to 40
 FT amino acids wherein each amino acid is independently
 FT selected from a group consisting of naturally occurring
 FT amino acids and amino acid mimetics"
 XX
 PN WO9835042-A2.
 XX
 PD 13-AUG-1998.
 XX
 PF 06-FEB-1998; 98WO-US002485.
 XX
 PR 07-FEB-1997; 97US-0037404P.
 XX
 PA (USSH) US SEC HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Brenneman DE, Bassan M;
 XX
 DR WPI; 1998-447239/38.
 XX
 PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excito-toxicity or Alzheimer's disease.
 XX
 PS Claim 24; Page 6; 121pp; English.
 XX
 CC This sequence represents a peptide used in a method which isolates a
 CC novel activity dependent neurotrophic factor III, ADNF-III (also known as
 CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
 CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurones associated with
 CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
 CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 1 NAPVSIPQ 8

RESULT 3
 AAY71143
 ID AAY71143 standard; peptide; 8 AA.
 XX
 AC AAY71143;

XX
DT 08-SEP-2000 (first entry)
XX
DE Human ADNF III-8 or NAP peptide sequence, NAPVSIPQ.
XX
KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP; NAP;
KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;
KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
KW Down's syndrome; drug addiction; developmental retardation; antilipemic;
KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.
XX
OS Homo sapiens.
XX
PN WO200027875-A2.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026213.
XX
PR 06-NOV-1998; 98US-00187330.
XX
PA (USAS) GOVERNMENT US REPRESENT AS.
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI Gozes I, Brenneman DE, Bassan M, Zamostiano R;
XX
DR WPI; 2000-376491/32.
XX
PT New nucleic acid encoding an activity dependent neurotrophic factor III
PT (ADNF III) useful in the treatment of neurological deficiencies and for
PT preventing neuronal cell death.
XX
PS Example; Page 5; 136pp; English.
XX
CC The present sequence is the human Activity Dependent Neurotrophic Factor
CC (ADNF) III-8 or NAP peptide sequence. This peptide was synthesised based
CC on the structural homology to ADNF-9 active peptide and hsp60. It is also
CC used as an antigen for immunological detection of cloned ADNF III. ADNF
CC III is also called an Activity Dependent Neuroprotective Protein (ADNP).
CC The human gene was mapped to chromosome 20q13.2 and is linked to
CC autosomal dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is
CC expressed in the astrocytes, brain and also in foetal lung and endocrine
CC tissues. This sequence has homology to ADNF I and hsp60, heat shock
CC protein and PIF1, a DNA repair protein. The ADNF III polypeptides are
CC useful for the treatment of neurological deficiencies and for prevention
CC of neuronal cell death associated with gp120, the envelope protein from
CC HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
CC of electrical activity); and beta-amyloid peptide, a substance related to
CC neuronal degeneration in Alzheimer's disease. It is useful for the
CC treatment of Huntington's disease, AIDS dementia complex, epilepsy,
CC neuropathic pain syndromes, Parkinson's disease, amyotrophic lateral

CC sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Wernicke's
CC encephalopathy, Alzheimer's disease, homocysteinuria, hyperprolinemia,
CC sulphite oxide disease, Tourette's syndrome, oxidative stress induced
CC neuronal death, Down's syndrome, developmental retardation and learning
CC impairments, drug addiction, tolerance and dependency
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 4

AAB23470

ID AAB23470 standard; peptide; 8 AA.

XX

AC AAB23470;

XX

DT 22-JAN-2001 (first entry)

XX

DE Activity dependent neurotrophic factor I peptide #2.

XX

KW Activity dependent neurotrophic factor; ADNF; FAS;

KW foetal alcohol syndrome; gene therapy; neurological deficiency;

KW neuronal cell death.

XX

OS Unidentified.

XX

PN WO200053217-A2.

XX

PD 14-SEP-2000.

XX

PF 10-MAR-2000; 2000WO-US006364.

XX

PR 12-MAR-1999; 99US-00267511.

XX

PA (UYRA-) UNIV RAMOT.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX

DR WPI; 2000-601940/57.

XX

PT Treating condition associated with fetal alcohol syndrome in a subject
PT exposed to alcohol in utero or reducing neuronal death, involves
PT administering activity dependent neurotrophic factors I and/or III.

XX

PS Claim 9; Page 51; 65pp; English.

XX

CC The present invention relates to the treatment of a condition associated
CC with foetal alcohol syndrome (FAS), involving administering an activity
CC dependent neurotropic factor (ADNF). ADNFs of the present invention may

CC also be used to treat neurological deficiencies and prevent neuronal cell
CC death. The present sequence is an ADNF peptide
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||||
Db 1 NAPVSIPQ 8

RESULT 5
AAB23472

ID AAB23472 standard; peptide; 8 AA.

XX

AC AAB23472;

XX

DT 22-JAN-2001 (first entry)

XX

DE Activity dependent neurotrophic factor I peptide #4.

XX

KW Activity dependent neurotrophic factor; ADNF; FAS;

KW foetal alcohol syndrome; gene therapy; neurological deficiency;

KW neuronal cell death.

XX

OS Unidentified.

XX

PN WO200053217-A2.

XX

PD 14-SEP-2000.

XX

PF 10-MAR-2000; 2000WO-US006364.

XX

PR 12-MAR-1999; 99US-00267511.

XX

PA (UYRA-) UNIV RAMOT.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX

DR WPI; 2000-601940/57.

XX

PT Treating condition associated with fetal alcohol syndrome in a subject

PT exposed to alcohol in utero or reducing neuronal death, involves

PT administering activity dependent neurotrophic factors I and/or III.

XX

PS Disclosure; Page 51; 65pp; English.

XX

CC The present invention relates to the treatment of a condition associated

CC with foetal alcohol syndrome (FAS), involving administering an activity

CC dependent neurotropic factor (ADNF). ADNFs of the present invention may

CC also be used to treat neurological deficiencies and prevent neuronal cell

CC death. The present sequence is an ADNF peptide

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 6

AAB72322

ID AAB72322 standard; peptide; 8 AA.

XX

AC AAB72322;

XX

DT 16-MAY-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 2.

XX

KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;

KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;

KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX

OS Synthetic.

XX

PN WO200112654-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022861.

XX

PR 18-AUG-1999; 99US-0149956P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;

XX

DR WPI; 2001-202855/20.

XX

PT Novel Activity Dependent Neurotrophic Factor I useful for treating
PT oxidative stress, reducing neuronal cell death and treating a condition
PT associated with fetal alcohol syndrome.

XX

PS Claim 10; Page 57; 88pp; English.

XX

CC This invention relates to an activity dependent neurotrophic factor I
CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC composition containing either ADNF I or ADNF III are useful for reducing
CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC neuronal cell death is associated with excito-toxicity induced by N-

CC methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
CC peptide in an Alzheimer's disease patient, or induced by cholinergic
CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC useful for treating oxidative stress in a patient, for reducing a
CC condition, such as decreased body weight, decreased brain weight,
CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC death, associated with foetal alcohol syndrome

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 1 NAPVSIPQ 8

RESULT 7

ABB07216

ID ABB07216 standard; peptide; 8 AA.

XX

AC ABB07216;

XX

DT 26-MAR-2002 (first entry)

XX

DE ADNF III polypeptide active core site peptide sequence.

XX

KW ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW NMDA receptor.

XX

OS Synthetic.

XX

PN WO200192333-A2.

XX

PD 06-DEC-2001.

XX

PF 31-MAY-2001; 2001WO-US017758.

XX

PR 31-MAY-2000; 2000US-0208944P.

PR

08-FEB-2001; 2001US-0267805P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Spong CY, Brenneman D, Gozes I;

XX

DR WPI; 2002-114330/15.

XX

PT Use of an activity dependent neurotrophic factor for improving learning
PT and/or memory in a subject by pre- or post-natal administration.

XX

PS Claim 1; Page 51; 80pp; English.

XX
 CC The invention provides a method of improving learning and/or memory in a
 CC subject that involves administering pre- or postnatally an Activity
 CC Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
 CC is an ADNF I and/or an ADNF III polypeptide comprising the core active
 CC site sequences ABB07215 or ABB07216. The method is useful for improving
 CC learning and/or memory in a subject; for treating a normal or old subject
 CC afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
 CC normal mental capacity, mental retardation, for the treatment of central
 CC motor systems including degenerative conditions affecting the basal
 CC ganglia (see ABB07215 for a detailed description of the various
 CC conditions that can be treated by using the ADNF polypeptides). The
 CC present sequence represents the active core site sequence of the ADNF III
 CC polypeptide
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 1 NAPVSIPQ 8

RESULT 8
 ABR39742
 ID ABR39742 standard; peptide; 8 AA.
 XX
 AC ABR39742;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 DE ADNP I active core peptide fragment NAP.
 XX
 KW ADNF I; Activity Dependent Neurotrophic Factor I; neuroprotective;
 KW anti-HIV; neuroleptic; antiparkinsonian; nootropic; ADNP; NAP; SAL;
 KW Activity Dependent Neuroprotective Protein.
 XX
 OS Unidentified.
 XX
 PN WO2003022226-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 12-SEP-2002; 2002WO-US029146.
 XX
 PR 12-SEP-2001; 2001US-0322760P.
 PR 10-APR-2002; 2002US-0371961P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brenneman DE, Castellon R, Spong CY, Hauser JM, Gozes I;
 XX
 DR WPI; 2003-354501/33.

XX
PT New Activity Dependent Neurotrophic Factor I complex polypeptide, useful
PT for reducing neuronal cell death, treating oxidative stress in a patient,
PT or improving learning and/or memory in a subject with e.g. Alzheimer's
PT disease.
XX
PS Disclosure; Page 2; 111pp; English.
XX
CC The invention relates to Activity Dependent Neurotrophic Factor I (ADNF
CC I) complex polypeptide selected from sequences ABR39744-754. The ADNF I
CC complex polypeptide is useful for reducing neuronal cell death in
CC conditions such as HIV infection, treating oxidative stress in a patient,
CC reducing a condition associated with fetal alcohol syndrome, or improving
CC learning and/or memory in a subject with e.g. Alzheimer's disease or
CC Down's syndrome. The ADNF complex polypeptides are also useful in
CC designing a drug treatment regime that can be individually tailored for
CC each patient affected by neurodegenerative disorders. The polypeptides
CC can also be used for diagnosing or treating Huntington's disease,
CC Wilson's disease, Parkinson's disease, AIDS-related dementia or
CC Tourette's syndrome. The present sequence represents a ADNP (activity
CC dependent neuroprotective protein) peptide, that has a biological
CC activity similar to a ADNF I peptide SAL
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||||
Db 1 NAPVSIPQ 8

RESULT 9
ADA07953
ID ADA07953 standard; peptide; 8 AA.
XX
AC ADA07953;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human activity dependent neuroprotective factor (ADNP) peptide #2.
XX
KW Human; glaucomatous optic neuropathy;
KW activity dependent neuroprotective factor; ADNP; ophthalmological.
XX
OS Homo sapiens.
XX
PN US2003166544-A1.
XX
PD 04-SEP-2003.
XX
PF 06-JUN-2002; 2002US-00164432.
XX
PR 07-SEP-2000; 2000US-0230964P.
PR 02-AUG-2001; 2001US-00921029.

XX
PA (CLAR/) CLARK A F.
PA (SHAD/) SHADE D L.
XX
PI Clark AF, Shade DL;
XX
DR WPI; 2003-720933/68.
XX
PT Treating glaucomatous optic neuropathy by administering a composition
PT comprising a peptide derived from or related to Activity Dependent
PT Neuroprotective Factor (ADNP).
XX
PS Claim 2; Page 2; 13pp; English.
XX
CC The present invention relates to a method for preventing and treating
CC glaucomatous optic neuropathy. The method comprises administering a
CC composition comprising a peptide derived from activity dependent
CC neuroprotective factor (ADNP). The method is useful for treating
CC glaucomatous optic neuropathy. The present sequence represents a peptide
CC from human ADNP.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||||
Db 1 NAPVSIPQ 8

RESULT 10

ADQ76121

ID ADQ76121 standard; peptide; 8 AA.

XX

AC ADQ76121;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:2.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.

XX

OS Synthetic.

XX
 PN WO2004060309-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 30-DEC-2003; 2003WO-US041540.
 XX
 PR 02-JAN-2003; 2003US-0437650P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
 XX
 DR WPI; 2004-543782/52.
 XX
 PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
 PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
 PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
 XX
 PS Claim 1; SEQ ID NO 2; 39pp; English.
 XX
 CC The present invention describes a method for preventing or treating an
 CC autoimmune disease in a subject. The method comprises administering an
 CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
 CC polypeptide is a member selected from the group consisting of: (a) an
 CC ADNF I polypeptide comprising an active core site with the amino acid
 CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
 CC comprising an active core site with the amino acid sequence of SEQ ID
 CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
 CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
 CC host cells, vectors and antibodies used in the methods are also disclosed
 CC in the present invention. ADNF sequences have immunosuppressive,
 CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
 CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
 CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
 CC activities, and can be used as neurotropic factor agonists. The methods
 CC and compositions of the present invention are useful for the prevention
 CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
 CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
 CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
 CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
 CC tissue disease, chronic active hepatitis, Graves'
 CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
 CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
 CC present sequence represents an ADNF III active core site peptide from the
 CC present invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 1 NAPVSIPQ 8

RESULT 11

ADS73609

ID ADS73609 standard; peptide; 8 AA.

XX

AC ADS73609;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III active core site.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;

KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises

PT administering an amount of an Activity Dependent Neurotrophic Factor

PT polypeptide to the subject.

XX

PS Claim 2; SEQ ID NO 2; 46pp; English.

XX

CC This sequence represents the active core peptide derived from Activity

CC Dependent Neurotrophic Factor (ADNF) III. This peptide may be used for

CC treating or preventing anxiety or depression in a subject. This sequence

CC may optionally be extended at either the N- and/or the C-terminals. The

CC ADNF polypeptide of the invention may be encoded by a nucleic acid that

CC is administered to the subject. It also contains a covalently bound

CC lipophilic moiety to enhance penetration or activity. The subject suffers

CC from anxiety or depression and the ADNF polypeptide is administered to

CC prevent anxiety or depression. The disease is selected from a panic

CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,

CC social phobia, social anxiety disorder, specific phobias, generalized

CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The

CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and

CC drugs that alleviate depression and provide neuroprotection.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 12

AAW64696

ID AAW64696 standard; protein; 10 AA.

XX

AC AAW64696;

XX

DT 17-OCT-2003 (revised)

DT 04-NOV-1998 (first entry)

XX

DE Seq ID 33 from WO9835042.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;

KW activity dependent neuroprotective protein; neurone; excito-toxicity;

KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;

KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;

KW HIV infection.

XX

OS unidentified.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.

XX

PA (USSH) US SEC HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Brenneman DE, Bassan M;

XX

DR WPI; 1998-447239/38.

XX

PT Activity dependent neurotrophic factor III polypeptide - useful

PT therapeutically to prevent neuronal cell death associated with e.g. HIV

PT infection, excito-toxicity or Alzheimer's disease.

XX

PS Disclosure; Page; 121pp; English.

XX

CC This specification describes the isolation of novel activity dependent

CC neurotrophic factor III, ADNF-III (also known as activity dependent

CC neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be

CC used to prevent neuronal cell death, of e.g. the spinal cord,

CC hippocampal, cerebral cortical or cholinergic neurones associated with

CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate

CC stimulation or beta-amyloid peptide in Alzheimer's disease. The

CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
 CC does not appear in the specification but is present in the Sequence ID
 CC listing. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 3 NAPVSIPQ 10

RESULT 13

AAY71139

ID AAY71139 standard; peptide; 10 AA.

XX

AC AAY71139;

XX

DT 08-SEP-2000 (first entry)

XX

DE Human Activity Dependent Neurotrophic Factor (ADNF) III generic peptide.

XX

KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP;
 KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;
 KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
 KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
 KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
 KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;
 KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
 KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
 KW Down's syndrome; drug addiction; developmental retardation; antilipemic;
 KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Xaa= (R1)x= N-terminal amino acid sequence
 FT comprising 1-40 residues, where x= one or zero"

FT Misc-difference 10

FT /note= "Xaa= (R2)y= C-terminal amino acid sequence
 FT comprising 1-40 residues, where y= one or zero"

XX

PN WO200027875-A2.

XX

PD 18-MAY-2000.

XX

PF 04-NOV-1999; 99WO-US026213.

XX

PR 06-NOV-1998; 98US-00187330.
 XX
 PA (USAS) GOVERNMENT US REPRESENT AS.
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Gozes I, Brenneman DE, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-376491/32.
 XX
 PT New nucleic acid encoding an activity dependent neurotrophic factor III
 PT (ADNF III) useful in the treatment of neurological deficiencies and for
 PT preventing neuronal cell death.
 XX
 PS Claim 25; Page 95; 136pp; English.
 XX
 CC The present sequence is the human Activity Dependent Neurotrophic Factor
 CC (ADNF) III generic peptide. It consists of the ADNF III-8 or NAP peptide,
 CC flanked by N- and C-terminal generic sites, comprising 1-40 amino acids.
 CC ADNF III is also called an Activity Dependent Neuroprotective Protein
 CC (ADNP). The human gene was mapped to chromosome 20q13.2 and is linked to
 CC autosomal dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is
 CC expressed in the astrocytes, brain and also in foetal lung and endocrine
 CC tissues. This sequence has homology to ADNF I and hsp60, heat shock
 CC protein and PIF1, a DNA repair protein. The ADNF III polypeptides are
 CC useful for the treatment of neurological deficiencies and for prevention
 CC of neuronal cell death associated with gp120, the envelope protein from
 CC HIV; N-methyl-D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage
 CC of electrical activity); and beta-amyloid peptide, a substance related to
 CC neuronal degeneration in Alzheimer's disease. It is useful for the
 CC treatment of Huntington's disease, AIDS dementia complex, epilepsy,
 CC neuropathic pain syndromes, Parkinson's disease, amyotrophic lateral
 CC sclerosis (ALS), mitochondrial abnormalities, Leber's disease, Wernicke's
 CC encephalopathy, Alzheimer's disease, homocysteinuria, hyperprolinemia,
 CC sulphite oxide disease, Tourette's syndrome, oxidative stress induced
 CC neuronal death, Down's syndrome, developmental retardation and learning
 CC impairments, drug addiction, tolerance and dependency
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 2 NAPVSIPQ 9

RESULT 14
 AAB23488
 ID AAB23488 standard; peptide; 10 AA.
 XX
 AC AAB23488;
 XX
 DT 14-MAY-2003 (revised)
 DT 22-JAN-2001 (first entry)
 XX

DE Activity dependent neurotrophic factor III peptide #1.
 XX
 KW Activity dependent neurotrophic factor; ADNF; FAS;
 KW foetal alcohol syndrome; gene therapy; neurological deficiency;
 KW neuronal cell death.
 XX
 OS Unidentified.
 XX
 PN WO200053217-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006364.
 XX
 PR 12-MAR-1999; 99US-00267511.
 XX
 PA (UYRA-) UNIV RAMOT.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-601940/57.
 XX
 PT Treating condition associated with fetal alcohol syndrome in a subject
 PT exposed to alcohol in utero or reducing neuronal death, involves
 PT administering activity dependent neurotrophic factors I and/or III.
 XX
 PS Claim 10; Page 4; 65pp; English.
 XX
 CC The present invention relates to the treatment of a condition associated
 CC with foetal alcohol syndrome (FAS), involving administering an activity
 CC dependent neurotropic factor (ADNF). ADNFs of the present invention may
 CC also be used to treat neurological deficiencies and prevent neuronal cell
 CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
 CC to correct PS field.)
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 3 NAPVSIPQ 10

RESULT 15

AAB72323

ID AAB72323 standard; peptide; 10 AA.

XX

AC AAB72323;

XX

DT 16-MAY-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 17.

XX

KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
 KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
 KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
 XX
 OS Synthetic.
 XX
 PN WO200112654-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022861.
 XX
 PR 18-AUG-1999; 99US-0149956P.
 XX
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
 XX
 DR WPI; 2001-202855/20.
 XX
 PT Novel Activity Dependent Neurotrophic Factor I useful for treating
 PT oxidative stress, reducing neuronal cell death and treating a condition
 PT associated with fetal alcohol syndrome.
 XX
 PS Claim 16; Page 57; 88pp; English.
 XX
 CC This invention relates to an activity dependent neurotrophic factor I
 CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
 CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
 CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
 CC composition containing either ADNF I or ADNF III are useful for reducing
 CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
 CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
 CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
 CC neuronal cell death is associated with excito-toxicity induced by N-
 CC methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
 CC peptide in an Alzheimer's disease patient, or induced by cholinergic
 CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
 CC useful for treating oxidative stress in a patient, for reducing a
 CC condition, such as decreased body weight, decreased brain weight,
 CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
 CC death, associated with foetal alcohol syndrome
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 3 NAPVSIPQ 10

RESULT 16
 AAB72328

ID AAB72328 standard; peptide; 10 AA.
XX
AC AAB72328;
XX
DT 16-MAY-2001 (first entry)
XX
DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 4.
XX
KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Optionally between 0 and 40 additional amino
FT acids"
FT Misc-difference 11
FT /note= "Optionally between 0 and 40 additional amino
FT acids"
XX
PN WO200112654-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022861.
XX
PR 18-AUG-1999; 99US-0149956P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
XX
DR WPI; 2001-202855/20.
XX
PT Novel Activity Dependent Neurotrophic Factor I useful for treating
PT oxidative stress, reducing neuronal cell death and treating a condition
PT associated with fetal alcohol syndrome.
XX
PS Disclosure; Page 24; 88pp; English.
XX
CC This invention relates to an activity dependent neurotrophic factor I
CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
CC composition containing either ADNF I or ADNF III are useful for reducing
CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
CC neuronal cell death is associated with excito-toxicity induced by N-
CC methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
CC peptide in an Alzheimer's disease patient, or induced by cholinergic
CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
CC useful for treating oxidative stress in a patient, for reducing a
CC condition, such as decreased body weight, decreased brain weight,

CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
CC death, associated with foetal alcohol syndrome. The present sequence
CC represents an example of an ADNF III peptide of the invention

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 2 NAPVSIPQ 9

RESULT 17

ABB07223

ID ABB07223 standard; peptide; 10 AA.

XX

AC ABB07223;

XX

DT 26-MAR-2002 (first entry)

XX

DE ADNF III polypeptide fragment comprising the active core site.

XX

KW ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW NMDA receptor.

XX

OS Synthetic.

XX

PN WO200192333-A2.

XX

PD 06-DEC-2001.

XX

PF 31-MAY-2001; 2001WO-US017758.

XX

PR 31-MAY-2000; 2000US-0208944P.

PR 08-FEB-2001; 2001US-0267805P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Spong CY, Brenneman D, Gozes I;

XX

DR WPI; 2002-114330/15.

XX

PT Use of an activity dependent neurotrophic factor for improving learning
PT and/or memory in a subject by pre- or post-natal administration.

XX

PS Claim 13; Page 52; 80pp; English.

XX

CC The invention provides a method of improving learning and/or memory in a
CC subject that involves administering pre- or postnatally an Activity
CC Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide

CC is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC site sequences ABB07215 or ABB07216. The method is useful for improving
CC learning and/or memory in a subject; for treating a normal or old subject
CC afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC normal mental capacity, mental retardation, for the treatment of central
CC motor systems including degenerative conditions affecting the basal
CC ganglia (see ABB07215 for a detailed description of the various
CC conditions that can be treated by using the ADNF polypeptides). Sequences
CC ABB07223-226 represent specific examples of ADNF III polypeptide
CC fragments which comprise the active core site in their sequence
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIPQ 8
|||
Db 3 NAPVSIPQ 10

RESULT 18

ADQ76135

ID ADQ76135 standard; peptide; 10 AA.

XX

AC ADQ76135;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:24.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;

KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;

KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;

KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;

KW antidiabetic; antibacterial; neurotropic factor agonist;

KW autoimmune disease; multiple sclerosis; myasthenia gravis;

KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;

KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;

KW hypothyroiditis; primary biliary cirrhosis;

KW mixed connective tissue disease; chronic active hepatitis;

KW Graves' disease; hyperthyroiditis; scleroderma;

KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;

KW septic shock.

XX

OS Synthetic.

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.

XX

PF 30-DEC-2003; 2003WO-US041540.

XX

PR 02-JAN-2003; 2003US-0437650P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
 XX
 DR WPI; 2004-543782/52.
 XX
 PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
 PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
 PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
 XX
 PS Claim 14; SEQ ID NO 2; 39pp; English.
 XX
 CC The present invention describes a method for preventing or treating an
 CC autoimmune disease in a subject. The method comprises administering an
 CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
 CC polypeptide is a member selected from the group consisting of: (a) an
 CC ADNF I polypeptide comprising an active core site with the amino acid
 CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
 CC comprising an active core site with the amino acid sequence of SEQ ID
 CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
 CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
 CC host cells, vectors and antibodies used in the methods are also disclosed
 CC in the present invention. ADNF sequences have immunosuppressive,
 CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
 CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
 CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
 CC activities, and can be used as neurotropic factor agonists. The methods
 CC and compositions of the present invention are useful for the prevention
 CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
 CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
 CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
 CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
 CC tissue disease, chronic active hepatitis, Graves'
 CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
 CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
 CC present sequence represents an ADNF III active core site peptide from the
 CC present invention.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIPQ 8
 |||||
 Db 3 NAPVSIPQ 10

RESULT 19
 ADQ76131
 ID ADQ76131 standard; peptide; 10 AA.
 XX
 AC ADQ76131;
 XX
 DT 07-OCT-2004 (first entry)
 XX

DE ADNF III active core site peptide SEQ ID NO:20.
XX
KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.
XX
OS Synthetic.
XX
PN WO2004060309-A2.
XX
PD 22-JUL-2004.
XX
PF 30-DEC-2003; 2003WO-US041540.
XX
PR 02-JAN-2003; 2003US-0437650P.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
XX
DR WPI; 2004-543782/52.
XX
PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
XX
PS Claim 21; SEQ ID NO 20; 39pp; English.
XX
CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,

CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 8; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 3 NAPVSIPQ 10

RESULT 20

ADQ76137

ID ADQ76137 standard; peptide; 10 AA.

XX

AC ADQ76137;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;

KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;

KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;

KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;

KW antidiabetic; antibacterial; neurotropic factor agonist;

KW autoimmune disease; multiple sclerosis; myasthenia gravis;

KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;

KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;

KW hypothyroiditis; primary biliary cirrhosis;

KW mixed connective tissue disease; chronic active hepatitis;

KW Graves' disease; hyperthyroiditis; scleroderma;

KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;

KW septic shock.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "X represents an amino acid sequence comprising

FT from 1 to 40 amino acids where each amino acid is

FT independently selected"

FT Misc-difference 10

FT /note= "X represents an amino acid sequence comprising

FT from 1 to 40 amino acids where each amino acid is

FT independently selected"

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.
 XX
 PF 30-DEC-2003; 2003WO-US041540.
 XX
 PR 02-JAN-2003; 2003US-0437650P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
 XX
 DR WPI; 2004-543782/52.
 XX
 PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
 PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
 PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
 XX
 PS Disclosure; Page 13; 39pp; English.
 XX
 CC The present invention describes a method for preventing or treating an
 CC autoimmune disease in a subject. The method comprises administering an
 CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
 CC polypeptide is a member selected from the group consisting of: (a) an
 CC ADNF I polypeptide comprising an active core site with the amino acid
 CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
 CC comprising an active core site with the amino acid sequence of SEQ ID
 CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
 CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
 CC host cells, vectors and antibodies used in the methods are also disclosed
 CC in the present invention. ADNF sequences have immunosuppressive,
 CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
 CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
 CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
 CC activities, and can be used as neurotropic factor agonists. The methods
 CC and compositions of the present invention are useful for the prevention
 CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
 CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
 CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
 CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
 CC tissue disease, chronic active hepatitis, Graves'
 CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
 CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
 CC present sequence represents an ADNF III active core site peptide from the
 CC present invention.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 2 NAPVSIPQ 9

RESULT 21

ADS73616

ID ADS73616 standard; peptide; 10 AA.

XX

AC ADS73616;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III polypeptide #1.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;

KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises

PT administering an amount of an Activity Dependent Neurotrophic Factor

PT polypeptide to the subject.

XX

PS Claim 17; SEQ ID NO 9; 46pp; English.

XX

CC This sequence represents a peptide based on Activity Dependent

CC Neurotrophic Factor (ADNF) III. This peptide may be used for treating or

CC preventing anxiety or depression in a subject. This sequence may

CC optionally be extended at either the N- and/or the C-terminals. The ADNF

CC polypeptide of the invention may be encoded by a nucleic acid that is

CC administered to the subject. It also contains a covalently bound

CC lipophilic moiety to enhance penetration or activity. The subject suffers

CC from anxiety or depression and the ADNF polypeptide is administered to

CC prevent anxiety or depression. The disease is selected from a panic

CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,

CC social phobia, social anxiety disorder, specific phobias, generalized

CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The

CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and

CC drugs that alleviate depression and provide neuroprotection.

XX

SQ Sequence 10 AA;

Query Match

100.0%; Score 41; DB 8; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 3 NAPVSIPQ 10

RESULT 22

ADS73620

ID ADS73620 standard; peptide; 10 AA.

XX

AC ADS73620;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III generic peptide.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;

KW neuroprotection.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1

FT /note= "1-40 amino acids"

FT Peptide 10

FT /note= "1-40 amino acids"

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises

PT administering an amount of an Activity Dependent Neurotrophic Factor

PT polypeptide to the subject.

XX

PS Claim 13; SEQ ID NO 13; 46pp; English.

XX

CC This sequence represents the generic peptide of the invention derived

CC from Activity Dependent Neurotrophic Factor (ADNF) III. This peptide may

CC be used for treating or preventing anxiety or depression in a subject.

CC This sequence may optionally be extended at either the N- and/or the C-
 CC terminals. The ADNF polypeptide of the invention may be encoded by a
 CC nucleic acid that is administered to the subject. It also contains a
 CC covalently bound lipophilic moiety to enhance penetration or activity.
 CC The subject suffers from anxiety or depression and the ADNF polypeptide
 CC is administered to prevent anxiety or depression. The disease is selected
 CC from a panic disorder, obsessive-compulsive disorder, post-traumatic
 CC stress disorder, social phobia, social anxiety disorder, specific
 CC phobias, generalized anxiety disorder, Major depression, dysthymia, and
 CC bipolar disorder. The NAP-tubulin binding site(s) is/are used to identify
 CC anxiolytic drugs and drugs that alleviate depression and provide
 CC neuroprotection.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 41; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 2 NAPVSIPQ 9

RESULT 23

AAW64697

ID AAW64697 standard; protein; 13 AA.

XX

AC AAW64697;

XX

DT 17-OCT-2003 (revised)

DT 04-NOV-1998 (first entry)

XX

DE Seq ID 34 from WO9835042.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
 KW activity dependent neuroprotective protein; neurone; excito-toxicity;
 KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
 KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
 KW HIV infection.

XX

OS unidentified.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.

XX

PA (USSH) US SEC HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Brenneman DE, Bassan M;

XX

DR WPI; 1998-447239/38.

XX

PT Activity dependent neurotrophic factor III polypeptide - useful
PT therapeutically to prevent neuronal cell death associated with e.g. HIV
PT infection, excito-toxicity or Alzheimer's disease.

XX

PS Disclosure; Page; 121pp; English.

XX

CC This specification describes the isolation of novel activity dependent
CC neurotrophic factor III, ADNF-III (also known as activity dependent
CC neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be
CC used to prevent neuronal cell death, of e.g. the spinal cord,
CC hippocampal, cerebral cortical or cholinergic neurones associated with
CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC polypeptides can also be combined with a carrier to alleviate learning
CC impairment produced by cholinergic blockage in Alzheimer's patients. The
CC nucleic acids are useful in polypeptide production and to detect ADNF III
CC polynucleotide in biological samples, while the antibodies are useful
CC therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
CC does not appear in the specification but is present in the Sequence ID
CC listing. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 4 NAPVSIPQ 11

RESULT 24

AAW64699

ID AAW64699 standard; protein; 13 AA.

XX

AC AAW64699;

XX

DT 17-OCT-2003 (revised)

DT 04-NOV-1998 (first entry)

XX

DE Seq ID 36 from WO9835042.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
KW activity dependent neuroprotective protein; neurone; excito-toxicity;
KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW HIV infection.

XX

OS unidentified.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.
 XX
 PA (USSH) US SEC HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Brenneman DE, Bassan M;
 XX
 DR WPI; 1998-447239/38.
 XX
 PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excito-toxicity or Alzheimer's disease.
 XX
 PS Disclosure; Page; 121pp; English.
 XX
 CC This specification describes the isolation of novel activity dependent
 CC neurotrophic factor III, ADNF-III (also known as activity dependent
 CC neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be
 CC used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurones associated with
 CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
 CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
 CC does not appear in the specification but is present in the Sequence ID
 CC listing. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 4 NAPVSIPQ 11

RESULT 25

AAB23489

ID AAB23489 standard; peptide; 13 AA.

XX

AC AAB23489;

XX

DT 14-MAY-2003 (revised)

DT 22-JAN-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III peptide #2.

XX

KW Activity dependent neurotrophic factor; ADNF; FAS;

KW foetal alcohol syndrome; gene therapy; neurological deficiency;

KW neuronal cell death.

XX

OS Unidentified.

XX

PN WO200053217-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US006364.
 XX
 PR 12-MAR-1999; 99US-00267511.
 XX
 PA (UYRA-) UNIV RAMOT.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-601940/57.
 XX
 PT Treating condition associated with fetal alcohol syndrome in a subject
 PT exposed to alcohol in utero or reducing neuronal death, involves
 PT administering activity dependent neurotrophic factors I and/or III.
 XX
 PS Claim 10; Page 4; 65pp; English.
 XX
 CC The present invention relates to the treatment of a condition associated
 CC with foetal alcohol syndrome (FAS), involving administering an activity
 CC dependent neurotropic factor (ADNF). ADNFs of the present invention may
 CC also be used to treat neurological deficiencies and prevent neuronal cell
 CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
 CC to correct PS field.)
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 4 NAPVSIPQ 11

RESULT 26

AAB72324

ID AAB72324 standard; peptide; 13 AA.

XX

AC AAB72324;

XX

DT 16-MAY-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 18.

XX

KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;

KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;

KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX

OS Synthetic.

XX

PN WO200112654-A2.

XX

PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022861.
 XX
 PR 18-AUG-1999; 99US-0149956P.
 XX
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Brennehan DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
 XX
 DR WPI; 2001-202855/20.
 XX
 PT Novel Activity Dependent Neurotrophic Factor I useful for treating
 PT oxidative stress, reducing neuronal cell death and treating a condition
 PT associated with fetal alcohol syndrome.
 XX
 PS Claim 16; Page 57; 88pp; English.
 XX
 CC This invention relates to an activity dependent neurotrophic factor I
 CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
 CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
 CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
 CC composition containing either ADNF I or ADNF III are useful for reducing
 CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
 CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
 CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
 CC neuronal cell death is associated with excito-toxicity induced by N-
 CC methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
 CC peptide in an Alzheimer's disease patient, or induced by cholinergic
 CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
 CC useful for treating oxidative stress in a patient, for reducing a
 CC condition, such as decreased body weight, decreased brain weight,
 CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
 CC death, associated with foetal alcohol syndrome
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 4 NAPVSIPQ 11

RESULT 27

ABB07224

ID ABB07224 standard; peptide; 13 AA.

XX

AC ABB07224;

XX

DT 26-MAR-2002 (first entry)

XX

DE ADNF III polypeptide fragment comprising the active core site.

XX

KW ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
KW antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
KW NMDA receptor.

XX
OS Synthetic.

XX
PN WO200192333-A2.

XX
PD 06-DEC-2001.

XX
PF 31-MAY-2001; 2001WO-US017758.

XX
PR 31-MAY-2000; 2000US-0208944P.

PR 08-FEB-2001; 2001US-0267805P.

XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Spong CY, Brenneman D, Gozes I;

XX
DR WPI; 2002-114330/15.

XX
PT Use of an activity dependent neurotropic factor for improving learning
PT and/or memory in a subject by pre- or post-natal administration.

XX
PS Claim 13; Page 52; 80pp; English.

XX
CC The invention provides a method of improving learning and/or memory in a
CC subject that involves administering pre- or postnatally an Activity
CC Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC site sequences ABB07215 or ABB07216. The method is useful for improving
CC learning and/or memory in a subject; for treating a normal or old subject
CC afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC normal mental capacity, mental retardation, for the treatment of central
CC motor systems including degenerative conditions affecting the basal
CC ganglia (see ABB07215 for a detailed description of the various
CC conditions that can be treated by using the ADNF polypeptides). Sequences
CC ABB07223-226 represent specific examples of ADNF III polypeptide
CC fragments which comprise the active core site in their sequence

XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 4 NAPVSIPQ 11

RESULT 28

ADQ76132

ID ADQ76132 standard; peptide; 13 AA.

XX
AC ADQ76132;
XX
DT 07-OCT-2004 (first entry)
XX
DE ADNF III active core site peptide SEQ ID NO:21.
XX
KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.
XX
OS Synthetic.
XX
PN WO2004060309-A2.
XX
PD 22-JUL-2004.
XX
PF 30-DEC-2003; 2003WO-US041540.
XX
PR 02-JAN-2003; 2003US-0437650P.
XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
XX
DR WPI; 2004-543782/52.
XX
PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
XX
PS Claim 21; SEQ ID NO 21; 39pp; English.
XX
CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,

CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 4 NAPVSIPQ 11

RESULT 29

ADQ76122

ID ADQ76122 standard; peptide; 13 AA.

XX

AC ADQ76122;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:3.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.

XX

OS Synthetic.

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.

XX

PF 30-DEC-2003; 2003WO-US041540.

XX

PR 02-JAN-2003; 2003US-0437650P.

XX
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
XX
DR WPI; 2004-543782/52.
XX
PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
XX
PS Claim 14; SEQ ID NO 3; 39pp; English.
XX
CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | | | | | |
Db 4 NAPVSIPQ 11

RESULT 30
ADS73632
ID ADS73632 standard; peptide; 13 AA.
XX
AC ADS73632;
XX

DT 16-DEC-2004 (first entry)
 XX
 DE Elongated NAP #2.
 XX
 KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;
 KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;
 KW activity; panic disorder; obsessive-compulsive disorder;
 KW post-traumatic stress disorder; social phobia; social anxiety disorder;
 KW specific phobia; generalized anxiety disorder; Major depression;
 KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;
 KW neuroprotection.
 XX
 OS Homo sapiens.
 XX
 PN WO2004080957-A2.
 XX
 PD 23-SEP-2004.
 XX
 PF 11-MAR-2004; 2004WO-IL000232.
 XX
 PR 12-MAR-2003; 2003US-0454505P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Gozes I, Alcalay RN, Divinski I, Giladi E;
 XX
 DR WPI; 2004-668930/65.
 XX
 PT Treating or preventing anxiety or depression in a subject comprises
 PT administering an amount of an Activity Dependent Neurotrophic Factor
 PT polypeptide to the subject.
 XX
 PS Example 2; SEQ ID NO 29; 46pp; English.
 XX
 CC This sequence represents an elongated NAP peptide, which is derived from
 CC the Activity Dependent Neurotrophic Factor (ADNF) III of the invention.
 CC The full length peptide may be used for treating or preventing anxiety or
 CC depression in a subject. This sequence may optionally be extended at
 CC either the N- and/or the C-terminals. The ADNF polypeptide of the
 CC invention may be encoded by a nucleic acid that is administered to the
 CC subject. It also contains a covalently bound lipophilic moiety to enhance
 CC penetration or activity. The subject suffers from anxiety or depression
 CC and the ADNF polypeptide is administered to prevent anxiety or
 CC depression. The disease is selected from a panic disorder, obsessive-
 CC compulsive disorder, post-traumatic stress disorder, social phobia,
 CC social anxiety disorder, specific phobias, generalized anxiety disorder,
 CC Major depression, dysthymia, and bipolar disorder. The NAP-tubulin
 CC binding site(s) is/are used to identify anxiolytic drugs and drugs that
 CC alleviate depression and provide neuroprotection.
 XX
 SQ Sequence 13 AA;

 Query Match 100.0%; Score 41; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

Db

|||||||
6 NAPVSIPQ 13

RESULT 31

ADS73617

ID ADS73617 standard; peptide; 13 AA.

XX

AC ADS73617;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III polypeptide #2.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;

KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises

PT administering an amount of an Activity Dependent Neurotrophic Factor

PT polypeptide to the subject.

XX

PS Claim 17; SEQ ID NO 10; 46pp; English.

XX

CC This sequence represents a peptide based on Activity Dependent

CC Neurotrophic Factor (ADNF) III. This peptide may be used for treating or

CC preventing anxiety or depression in a subject. This sequence may

CC optionally be extended at either the N- and/or the C-terminals. The ADNF

CC polypeptide of the invention may be encoded by a nucleic acid that is

CC administered to the subject. It also contains a covalently bound

CC lipophilic moiety to enhance penetration or activity. The subject suffers

CC from anxiety or depression and the ADNF polypeptide is administered to

CC prevent anxiety or depression. The disease is selected from a panic

CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,

CC social phobia, social anxiety disorder, specific phobias, generalized

CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The

CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and

CC drugs that alleviate depression and provide neuroprotection.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 41; DB 8; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 4 NAPVSIPQ 11

RESULT 32

ADS73631

ID ADS73631 standard; peptide; 14 AA.

XX

AC ADS73631;

XX

DT 16-DEC-2004 (first entry)

XX

DE Elongated NAP.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;

KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises

PT administering an amount of an Activity Dependent Neurotrophic Factor

PT polypeptide to the subject.

XX

PS Example 2; SEQ ID NO 28; 46pp; English.

XX

CC This sequence represents an elongated NAP peptide, which is derived from
CC the Activity Dependent Neurotrophic Factor (ADNF) III of the invention.

CC The full length peptide may be used for treating or preventing anxiety or
CC depression in a subject. This sequence may optionally be extended at

CC either the N- and/or the C-terminals. The ADNF polypeptide of the
CC invention may be encoded by a nucleic acid that is administered to the
CC subject. It also contains a covalently bound lipophilic moiety to enhance
CC penetration or activity. The subject suffers from anxiety or depression
CC and the ADNF polypeptide is administered to prevent anxiety or
CC depression. The disease is selected from a panic disorder, obsessive-
CC compulsive disorder, post-traumatic stress disorder, social phobia,
CC social anxiety disorder, specific phobias, generalized anxiety disorder,
CC Major depression, dysthymia, and bipolar disorder. The NAP-tubulin
CC binding site(s) is/are used to identify anxiolytic drugs and drugs that
CC alleviate depression and provide neuroprotection.

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 41; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 33

AAW64698

ID AAW64698 standard; protein; 15 AA.

XX

AC AAW64698;

XX

DT 17-OCT-2003 (revised)

DT 04-NOV-1998 (first entry)

XX

DE Seq ID 35 from WO9835042.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
KW activity dependent neuroprotective protein; neurone; excito-toxicity;
KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW HIV infection.

XX

OS unidentified.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.

XX

PA (USSH) US SEC HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Brenneman DE, Bassan M;

XX

DR WPI; 1998-447239/38.

XX

PT Activity dependent neurotrophic factor III polypeptide - useful

PT therapeutically to prevent neuronal cell death associated with e.g. HIV
PT infection, excito-toxicity or Alzheimer's disease.

XX

PS Disclosure; Page; 121pp; English.

XX

CC This specification describes the isolation of novel activity dependent
CC neurotrophic factor III, ADNF-III (also known as activity dependent
CC neuroprotective protein, ADNP) sequences. ADNF III polypeptides can be
CC used to prevent neuronal cell death, of e.g. the spinal cord,
CC hippocampal, cerebral cortical or cholinergic neurones associated with
CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
CC polypeptides can also be combined with a carrier to alleviate learning
CC impairment produced by cholinergic blockage in Alzheimer's patients. The
CC nucleic acids are useful in polypeptide production and to detect ADNF III
CC polynucleotide in biological samples, while the antibodies are useful
CC therapeutically and to isolate ADNF III polypeptides. NOTE: This sequence
CC does not appear in the specification but is present in the Sequence ID
CC listing. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 34

AAB23490

ID AAB23490 standard; peptide; 15 AA.

XX

AC AAB23490;

XX

DT 14-MAY-2003 (revised)

DT 22-JAN-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III peptide #3.

XX

KW Activity dependent neurotrophic factor; ADNF; FAS;
KW foetal alcohol syndrome; gene therapy; neurological deficiency;
KW neuronal cell death.

XX

OS Unidentified.

XX

PN WO200053217-A2.

XX

PD 14-SEP-2000.

XX

PF 10-MAR-2000; 2000WO-US006364.

XX

PR 12-MAR-1999; 99US-00267511.

XX

PA (UYRA-) UNIV RAMOT.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX

DR WPI; 2000-601940/57.

XX

PT Treating condition associated with fetal alcohol syndrome in a subject
PT exposed to alcohol in utero or reducing neuronal death, involves
PT administering activity dependent neurotrophic factors I and/or III.

XX

PS Claim 10; Page 4; 65pp; English.

XX

CC The present invention relates to the treatment of a condition associated
CC with foetal alcohol syndrome (FAS), involving administering an activity
CC dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC also be used to treat neurological deficiencies and prevent neuronal cell
CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
CC to correct PS field.)

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 6 NAPVSIPQ 13

RESULT 35

AAB72325

ID AAB72325 standard; peptide; 15 AA.

XX

AC AAB72325;

XX

DT 16-MAY-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 22.

XX

KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX

OS Synthetic.

XX

PN WO200112654-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022861.

XX

PR 18-AUG-1999; 99US-0149956P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;
 XX
 DR WPI; 2001-202855/20.
 XX
 PT Novel Activity Dependent Neurotrophic Factor I useful for treating
 PT oxidative stress, reducing neuronal cell death and treating a condition
 PT associated with fetal alcohol syndrome.
 XX
 PS Claim 16; Page 57; 88pp; English.
 XX
 CC This invention relates to an activity dependent neurotrophic factor I
 CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
 CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
 CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
 CC composition containing either ADNF I or ADNF III are useful for reducing
 CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
 CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
 CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
 CC neuronal cell death is associated with excito-toxicity induced by N-
 CC methyl-D-aspartate (NMDA) stimulation, which is induced by beta-amyloid
 CC peptide in an Alzheimer's disease patient, or induced by cholinergic
 CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
 CC useful for treating oxidative stress in a patient, for reducing a
 CC condition, such as decreased body weight, decreased brain weight,
 CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
 CC death, associated with foetal alcohol syndrome
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 6 NAPVSIPQ 13

RESULT 36

ABB07225

ID ABB07225 standard; peptide; 15 AA.

XX

AC ABB07225;

XX

DT 26-MAR-2002 (first entry)

XX

DE ADNF III polypeptide fragment comprising the active core site.

XX

KW ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
 KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
 KW antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
 KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
 KW NMDA receptor.

XX

OS Synthetic.

XX

PN WO200192333-A2.

XX
PD 06-DEC-2001.
XX
PF 31-MAY-2001; 2001WO-US017758.
XX
PR 31-MAY-2000; 2000US-0208944P.
PR 08-FEB-2001; 2001US-0267805P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Spong CY, Brenneman D, Gozes I;
XX
DR WPI; 2002-114330/15.
XX
PT Use of an activity dependent neurotropic factor for improving learning
PT and/or memory in a subject by pre- or post-natal administration.
XX
PS Claim 13; Page 52; 80pp; English.
XX
CC The invention provides a method of improving learning and/or memory in a
CC subject that involves administering pre- or postnatally an Activity
CC Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
CC is an ADNF I and/or an ADNF III polypeptide comprising the core active
CC site sequences ABB07215 or ABB07216. The method is useful for improving
CC learning and/or memory in a subject; for treating a normal or old subject
CC afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
CC normal mental capacity, mental retardation, for the treatment of central
CC motor systems including degenerative conditions affecting the basal
CC ganglia (see ABB07215 for a detailed description of the various
CC conditions that can be treated by using the ADNF polypeptides). Sequences
CC ABB07223-226 represent specific examples of ADNF III polypeptide
CC fragments which comprise the active core site in their sequence
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
| | | | | | | |
Db 6 NAPVSIPO 13

RESULT 37

ADQ76123

ID ADQ76123 standard; peptide; 15 AA.

XX

AC ADQ76123;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:4.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;

KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;

KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.

XX

OS Synthetic.

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.

XX

PF 30-DEC-2003; 2003WO-US041540.

XX

PR 02-JAN-2003; 2003US-0437650P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;

XX

DR WPI; 2004-543782/52.

XX

PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.

XX

PS Claim 14; SEQ ID NO 4; 39pp; English.

XX

CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic

CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 38

ADQ76133

ID ADQ76133 standard; peptide; 15 AA.

XX

AC ADQ76133;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:22.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
KW antidiabetic; antibacterial; neurotropic factor agonist;
KW autoimmune disease; multiple sclerosis; myasthenia gravis;
KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
KW hypothyroiditis; primary biliary cirrhosis;
KW mixed connective tissue disease; chronic active hepatitis;
KW Graves' disease; hyperthyroiditis; scleroderma;
KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
KW septic shock.

XX

OS Synthetic.

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.

XX

PF 30-DEC-2003; 2003WO-US041540.

XX

PR 02-JAN-2003; 2003US-0437650P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;

XX

DR WPI; 2004-543782/52.

XX

PT Preventing or treating autoimmune diseases, such as multiple sclerosis,

PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.

XX

PS Claim 21; SEQ ID NO 22; 39pp; English.

XX

CC The present invention describes a method for preventing or treating an
CC autoimmune disease in a subject. The method comprises administering an
CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
CC polypeptide is a member selected from the group consisting of: (a) an
CC ADNF I polypeptide comprising an active core site with the amino acid
CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 39

ADS73618

ID ADS73618 standard; peptide; 15 AA.

XX

AC ADS73618;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III polypeptide #3.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;

KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;

KW activity; panic disorder; obsessive-compulsive disorder;

KW post-traumatic stress disorder; social phobia; social anxiety disorder;

KW specific phobia; generalized anxiety disorder; Major depression;

KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;
KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX

PI Gozes I, Alcalay RN, Divinski I, Giladi E;

XX

DR WPI; 2004-668930/65.

XX

PT Treating or preventing anxiety or depression in a subject comprises
PT administering an amount of an Activity Dependent Neurotrophic Factor
PT polypeptide to the subject.

XX

PS Claim 17; SEQ ID NO 11; 46pp; English.

XX

CC This sequence represents a peptide based on Activity Dependent
CC Neurotrophic Factor (ADNF) III. This peptide may be used for treating or
CC preventing anxiety or depression in a subject. This sequence may
CC optionally be extended at either the N- and/or the C-terminals. The ADNF
CC polypeptide of the invention may be encoded by a nucleic acid that is
CC administered to the subject. It also contains a covalently bound
CC lipophilic moiety to enhance penetration or activity. The subject suffers
CC from anxiety or depression and the ADNF polypeptide is administered to
CC prevent anxiety or depression. The disease is selected from a panic
CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,
CC social phobia, social anxiety disorder, specific phobias, generalized
CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The
CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and
CC drugs that alleviate depression and provide neuroprotection.

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 41; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 6 NAPVSIPQ 13

RESULT 40

AAW64680

ID AAW64680 standard; protein; 18 AA.

XX

AC AAW64680;

XX

DT 04-NOV-1998 (first entry)
 XX
 DE Human ADNF-III assay inactive control peptide.
 XX
 KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;
 KW activity dependent neuroprotective protein; neurone; excito-toxicity;
 KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
 KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
 KW HIV infection.
 XX
 OS Synthetic.
 XX
 PN WO9835042-A2.
 XX
 PD 13-AUG-1998.
 XX
 PF 06-FEB-1998; 98WO-US002485.
 XX
 PR 07-FEB-1997; 97US-0037404P.
 XX
 PA (USSH) US SEC HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Brenneman DE, Bassan M;
 XX
 DR WPI; 1998-447239/38.
 XX
 PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excito-toxicity or Alzheimer's disease.
 XX
 PS Example 4d; Page 10; 121pp; English.
 XX
 CC This sequence represents a peptide used in a method which isolates a
 CC novel activity dependent neurotrophic factor III, ADNF-III (also known as
 CC activity dependent neuroprotective protein, ADNP). ADNF III polypeptides
 CC can be used to prevent neuronal cell death, of e.g. the spinal cord,
 CC hippocampal, cerebral cortical or cholinergic neurones associated with
 CC e.g. HIV infection, excito-toxicity induced by N-methyl-D-aspartate
 CC stimulation or beta-amyloid peptide in Alzheimer's disease. The
 CC polypeptides can also be combined with a carrier to alleviate learning
 CC impairment produced by cholinergic blockage in Alzheimer's patients. The
 CC nucleic acids are useful in polypeptide production and to detect ADNF III
 CC polynucleotide in biological samples, while the antibodies are useful
 CC therapeutically and to isolate ADNF III polypeptides
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 9 NAPVSIPQ 16

RESULT 41

AAAY71145

ID AAY71145 standard; peptide; 18 AA.

XX

AC AAY71145;

XX

DT 08-SEP-2000 (first entry)

XX

DE Inactive control peptide for ADNF III biological activity assessment.

XX

KW Activity Dependent Neurotrophic Factor III; ADNF; chromosome 20q13.2;

KW ADNP; Activity Dependent Neuroprotective Protein; neuronal cell death;

KW ADNFLE; autosomal dominant nocturnal frontal-lobe epilepsy; HIV;

KW Human Immunodeficiency Virus; neurological deficiency; treatment;

KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;

KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;

KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;

KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;

KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;

KW Down's syndrome; drug addiction; developmental retardation; antilipemic;

KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.

XX

OS Unidentified.

XX

PN WO200027875-A2.

XX

PD 18-MAY-2000.

XX

PF 04-NOV-1999; 99WO-US026213.

XX

PR 06-NOV-1998; 98US-00187330.

XX

PA (USAS) GOVERNMENT US REPRESENT AS.

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX

PI Gozes I, Brenneman DE, Bassan M, Zamostiano R;

XX

DR WPI; 2000-376491/32.

XX

PT New nucleic acid encoding an activity dependent neurotrophic factor III

PT (ADNF III) useful in the treatment of neurological deficiencies and for

PT preventing neuronal cell death.

XX

PS Disclosure; Page 11; 136pp; English.

XX

CC The present sequence is the inactive control peptide, used for biological
CC activity assessment of Activity Dependent Neurotrophic Factor (ADNF)-III,
CC from cerebral cortical cultures derived from newborn rats. ADNF III is
CC also called an Activity Dependent Neuroprotective Protein (ADNP). The
CC human gene was mapped to chromosome 20q13.2 and is linked to autosomal
CC dominant nocturnal frontal-lobe epilepsy (ADNFLE) gene. It is expressed
CC in the astrocytes, brain and also in foetal lung and endocrine tissues.
CC This sequence has homology to ADNF I and hsp60, heat shock protein and
CC PIF1, a DNA repair protein. The ADNF III polypeptides are useful for the
CC treatment of neurological deficiencies and for prevention of neuronal
CC cell death associated with gp120, the envelope protein from HIV; N-methyl
CC -D-Aspartic acid (excito-toxicity); tetrodotoxin (blockage of electrical
CC activity); and beta-amyloid peptide, a substance related to neuronal

CC degeneration in Alzheimer's disease. It is useful for the treatment of
CC Huntington's disease, AIDS dementia complex, epilepsy, neuropathic pain
CC syndromes, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
CC mitochondrial abnormalities, Leber's disease, Wernicke's encephalopathy,
CC Alzheimer's disease, homocysteinuria, hyperprolinemia, sulphite oxide
CC disease, Tourette's syndrome, oxidative stress induced neuronal death,
CC Down's syndrome, developmental retardation and learning impairments, drug
CC addiction, tolerance and dependency

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

|||||||

Db 9 NAPVSIPQ 16

RESULT 42

AAB23491

ID AAB23491 standard; peptide; 18 AA.

XX

AC AAB23491;

XX

DT 14-MAY-2003 (revised)

DT 22-JAN-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III peptide #4.

XX

KW Activity dependent neurotrophic factor; ADNF; FAS;

KW foetal alcohol syndrome; gene therapy; neurological deficiency;

KW neuronal cell death.

XX

OS Unidentified.

XX

PN WO200053217-A2.

XX

PD 14-SEP-2000.

XX

PF 10-MAR-2000; 2000WO-US006364.

XX

PR 12-MAR-1999; 99US-00267511.

XX

PA (UYRA-) UNIV RAMOT.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Spong CY, Gozes I, Bassan M, Zamostiano R;

XX

DR WPI; 2000-601940/57.

XX

PT Treating condition associated with fetal alcohol syndrome in a subject

PT exposed to alcohol in utero or reducing neuronal death, involves

PT administering activity dependent neurotrophic factors I and/or III.

XX

PS Claim 10; Page 4; 65pp; English.

XX
CC The present invention relates to the treatment of a condition associated
CC with foetal alcohol syndrome (FAS), involving administering an activity
CC dependent neurotropic factor (ADNF). ADNFs of the present invention may
CC also be used to treat neurological deficiencies and prevent neuronal cell
CC death. The present sequence is an ADNF peptide. (Updated on 14-MAY-2003
CC to correct PS field.)
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 9 NAPVSIPQ 16

RESULT 43

AAB72326

ID AAB72326 standard; peptide; 18 AA.

XX

AC AAB72326;

XX

DT 16-MAY-2001 (first entry)

XX

DE Activity dependent neurotrophic factor III (ADNF III) peptide SEQ ID 23.

XX

KW Activity dependent neurotrophic factor I; ADNF I; ADNF III; body weight;
KW neuronal cell death; Alzheimer's disease; oxidative stress; VIP;
KW vasoactive intestinal peptide; foetal death; foetal alcohol syndrome.

XX

OS Synthetic.

XX

PN WO200112654-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022861.

XX

PR 18-AUG-1999; 99US-0149956P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Brenneman DE, Gozes I, Spong CY, Pinhasov A, Giladi E;

XX

DR WPI; 2001-202855/20.

XX

PT Novel Activity Dependent Neurotrophic Factor I useful for treating
PT oxidative stress, reducing neuronal cell death and treating a condition
PT associated with fetal alcohol syndrome.

XX

PS Claim 16; Page 57; 88pp; English.

XX

CC This invention relates to an activity dependent neurotrophic factor I

CC (ADNF I) or ADNF III polypeptide. Sequences AAB72315 - AAB72321 represent
 CC ADNF I active core site peptides. Sequences AAB72322 - AAB72326 represent
 CC ADNF III active core site peptides. ADNF I, ADNF III and a pharmaceutical
 CC composition containing either ADNF I or ADNF III are useful for reducing
 CC neuronal cell death, e.g. death of spinal cord neurons, hippocampal
 CC neurons, cerebral cortical neurons and cholinergic neurons, in a patient
 CC infected with a virus, e.g. human immunodeficiency virus (HIV). The
 CC neuronal cell death is associated with excito-toxicity induced by N-
 CC methyl-D-aspartate (NMDE) stimulation, which is induced by beta-amyloid
 CC peptide in an Alzheimer's disease patient, or induced by cholinergic
 CC blockade. ADNF I, ADNF III and the pharmaceutical composition are also
 CC useful for treating oxidative stress in a patient, for reducing a
 CC condition, such as decreased body weight, decreased brain weight,
 CC decreased level of vasoactive intestinal peptide (VIP) mRNA, and foetal
 CC death, associated with foetal alcohol syndrome
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 9 NAPVSIPQ 16

RESULT 44

ABB07226

ID ABB07226 standard; peptide; 18 AA.

XX

AC ABB07226;

XX

DT 26-MAR-2002 (first entry)

XX

DE ADNF III polypeptide fragment comprising the active core site.

XX

KW ADNF; Activity Dependent Neurotrophic Factor; nootropic; neuroprotective;
 KW cerebroprotective; antidiabetic; neuroleptic; anticonvulsant; anti-HIV;
 KW antiparkinsonian; tranquilizer; antialcoholic; vulnerary; antibacterial;
 KW antiinflammatory; antidote; ophthalmological; muscular; vasodilator;
 KW NMDA receptor.

XX

OS Synthetic.

XX

PN WO200192333-A2.

XX

PD 06-DEC-2001.

XX

PF 31-MAY-2001; 2001WO-US017758.

XX

PR 31-MAY-2000; 2000US-0208944P.

PR 08-FEB-2001; 2001US-0267805P.

XX

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Spong CY, Brennehan D, Gozes I;
 XX
 DR WPI; 2002-114330/15.
 XX
 PT Use of an activity dependent neurotropic factor for improving learning
 PT and/or memory in a subject by pre- or post-natal administration.
 XX
 PS Claim 13; Page 52; 80pp; English.
 XX
 CC The invention provides a method of improving learning and/or memory in a
 CC subject that involves administering pre- or postnatally an Activity
 CC Dependent Neurotrophic Factor (ADNF) to the subject. The ADNF polypeptide
 CC is an ADNF I and/or an ADNF III polypeptide comprising the core active
 CC site sequences ABB07215 or ABB07216. The method is useful for improving
 CC learning and/or memory in a subject; for treating a normal or old subject
 CC afflicted with neuropathology, Alzheimer's disease, Down's syndrome,
 CC normal mental capacity, mental retardation, for the treatment of central
 CC motor systems including degenerative conditions affecting the basal
 CC ganglia (see ABB07215 for a detailed description of the various
 CC conditions that can be treated by using the ADNF polypeptides). Sequences
 CC ABB07223-226 represent specific examples of ADNF III polypeptide
 CC fragments which comprise the active core site in their sequence
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 9 NAPVSIPQ 16

RESULT 45

ADQ76134

ID ADQ76134 standard; peptide; 18 AA.

XX

AC ADQ76134;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:23.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;
 KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;
 KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;
 KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;
 KW antidiabetic; antibacterial; neurotropic factor agonist;
 KW autoimmune disease; multiple sclerosis; myasthenia gravis;
 KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;
 KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;
 KW hypothyroiditis; primary biliary cirrhosis;
 KW mixed connective tissue disease; chronic active hepatitis;
 KW Graves' disease; hyperthyroiditis; scleroderma;
 KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;
 KW septic shock.

XX
 OS Synthetic.
 XX
 PN WO2004060309-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 30-DEC-2003; 2003WO-US041540.
 XX
 PR 02-JAN-2003; 2003US-0437650P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;
 XX
 DR WPI; 2004-543782/52.
 XX
 PT Preventing or treating autoimmune diseases, such as multiple sclerosis,
 PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic
 PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.
 XX
 PS Claim 21; SEQ ID NO 23; 39pp; English.
 XX
 CC The present invention describes a method for preventing or treating an
 CC autoimmune disease in a subject. The method comprises administering an
 CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF
 CC polypeptide is a member selected from the group consisting of: (a) an
 CC ADNF I polypeptide comprising an active core site with the amino acid
 CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide
 CC comprising an active core site with the amino acid sequence of SEQ ID
 CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
 CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
 CC host cells, vectors and antibodies used in the methods are also disclosed
 CC in the present invention. ADNF sequences have immunosuppressive,
 CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
 CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
 CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
 CC activities, and can be used as neurotropic factor agonists. The methods
 CC and compositions of the present invention are useful for the prevention
 CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
 CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
 CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
 CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
 CC tissue disease, chronic active hepatitis, Graves'
 CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
 CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
 CC present sequence represents an ADNF III active core site peptide from the
 CC present invention.
 XX
 SQ Sequence 18 AA;

 Query Match 100.0%; Score 41; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

Db

|||||||
9 NAPVSIPQ 16

RESULT 46

ADQ76124

ID ADQ76124 standard; peptide; 18 AA.

XX

AC ADQ76124;

XX

DT 07-OCT-2004 (first entry)

XX

DE ADNF III active core site peptide SEQ ID NO:5.

XX

KW activity dependent neurotropic factor; ADNF; ADNF III; active core site;

KW immunosuppressive; nootropic; neuroprotective; antiinflammatory;

KW vasotropic; muscular; CNS; thyromimetic; antithyroid; antirheumatic;

KW antiarthritic; hepatotropic; virucide; dermatological; haemostatic;

KW antidiabetic; antibacterial; neurotropic factor agonist;

KW autoimmune disease; multiple sclerosis; myasthenia gravis;

KW Guillain-Barre syndrome; systemic lupus erythematosus; Behcet's syndrome;

KW Sjogren's syndrome; rheumatoid arthritis; Hashimoto's disease;

KW hypothyroiditis; primary biliary cirrhosis;

KW mixed connective tissue disease; chronic active hepatitis;

KW Graves' disease; hyperthyroiditis; scleroderma;

KW chronic idiopathic thrombocytopenic purpura; diabetic neuropathy;

KW septic shock.

XX

OS Synthetic.

XX

PN WO2004060309-A2.

XX

PD 22-JUL-2004.

XX

PF 30-DEC-2003; 2003WO-US041540.

XX

PR 02-JAN-2003; 2003US-0437650P.

XX

PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Gozes I, Offen D, Giladi E, Melamed E, Brenneman D;

XX

DR WPI; 2004-543782/52.

XX

PT Preventing or treating autoimmune diseases, such as multiple sclerosis,

PT rheumatoid arthritis, hepatitis, Graves' disease, scleroderma and septic

PT shock, using an Activity Dependent Neurotropic Factor (ADNF) polypeptide.

XX

PS Claim 14; SEQ ID NO 5; 39pp; English.

XX

CC The present invention describes a method for preventing or treating an

CC autoimmune disease in a subject. The method comprises administering an

CC activity dependent neurotropic factor (ADNF) polypeptide, where the ADNF

CC polypeptide is a member selected from the group consisting of: (a) an

CC ADNF I polypeptide comprising an active core site with the amino acid

CC sequence of SEQ ID NO:1 (ADQ76120); (b) an ADNF III polypeptide

CC comprising an active core site with the amino acid sequence of SEQ ID
CC NO:2 (ADQ76121); and (c) a mixture of the ADNF I polypeptide of part (a)
CC and the ADNF III polypeptide of part (b). ADNF-encoding nucleic acids,
CC host cells, vectors and antibodies used in the methods are also disclosed
CC in the present invention. ADNF sequences have immunosuppressive,
CC nootropic, neuroprotective, antiinflammatory, vasotropic, muscular, CNS,
CC thyromimetic, antithyroid, antirheumatic, antiarthritic, hepatotropic,
CC virucide, dermatological, haemostatic, antidiabetic and antibacterial
CC activities, and can be used as neurotropic factor agonists. The methods
CC and compositions of the present invention are useful for the prevention
CC and/or treatment of autoimmune diseases, such as multiple sclerosis,
CC myasthenia gravis, Guillain-Barre syndrome, systemic lupus erythematosus,
CC Behcet's syndrome, Sjogren's syndrome, rheumatoid arthritis, Hashimoto's
CC disease/hypothyroiditis, primary biliary cirrhosis, mixed connective
CC tissue disease, chronic active hepatitis, Graves'
CC disease/hyperthyroiditis, scleroderma, chronic idiopathic
CC thrombocytopenic purpura, diabetic neuropathy and septic shock. The
CC present sequence represents an ADNF III active core site peptide from the
CC present invention.

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 9 NAPVSIPQ 16

RESULT 47

ADS73619

ID ADS73619 standard; peptide; 18 AA.

XX

AC ADS73619;

XX

DT 16-DEC-2004 (first entry)

XX

DE ADNF III polypeptide #4.

XX

KW active; core peptide; Activity Dependent Neurotrophic Factor; ADNF;
KW ADNF I; ADNF III; anxiety; depression; lipophilic moiety; penetration;
KW activity; panic disorder; obsessive-compulsive disorder;
KW post-traumatic stress disorder; social phobia; social anxiety disorder;
KW specific phobia; generalized anxiety disorder; Major depression;
KW dysthymia; bipolar disorder; NAP-tubulin; binding site; anxiolytic drug;
KW neuroprotection.

XX

OS Homo sapiens.

XX

PN WO2004080957-A2.

XX

PD 23-SEP-2004.

XX

PF 11-MAR-2004; 2004WO-IL000232.

XX

PR 12-MAR-2003; 2003US-0454505P.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Gozes I, Alcalay RN, Divinski I, Giladi E;
 XX
 DR WPI; 2004-668930/65.
 XX
 PT Treating or preventing anxiety or depression in a subject comprises
 PT administering an amount of an Activity Dependent Neurotrophic Factor
 PT polypeptide to the subject.
 XX
 PS Claim 17; SEQ ID NO 12; 46pp; English.
 XX
 CC This sequence represents a peptide based on Activity Dependent
 CC Neurotrophic Factor (ADNF) III. This peptide may be used for treating or
 CC preventing anxiety or depression in a subject. This sequence may
 CC optionally be extended at either the N- and/or the C-terminals. The ADNF
 CC polypeptide of the invention may be encoded by a nucleic acid that is
 CC administered to the subject. It also contains a covalently bound
 CC lipophilic moiety to enhance penetration or activity. The subject suffers
 CC from anxiety or depression and the ADNF polypeptide is administered to
 CC prevent anxiety or depression. The disease is selected from a panic
 CC disorder, obsessive-compulsive disorder, post-traumatic stress disorder,
 CC social phobia, social anxiety disorder, specific phobias, generalized
 CC anxiety disorder, Major depression, dysthymia, and bipolar disorder. The
 CC NAP-tubulin binding site(s) is/are used to identify anxiolytic drugs and
 CC drugs that alleviate depression and provide neuroprotection.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 41; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 9 NAPVSIPQ 16

RESULT 48

AAAY71137

ID AAY71137 standard; protein; 726 AA.

XX

AC AAY71137;

XX

DT 08-SEP-2000 (first entry)

XX

DE Human Activity Dependent Neurotrophic Factor (ADNF) III H3 protein.

XX

KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP;

KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;

KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;

KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;

KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;

KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;

KW amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;

KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;
 KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;
 KW Down's syndrome; drug addiction; developmental retardation; antilipemic;
 KW learning impairment; anticonvulsant; neuroprotective; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 57. .65
 FT /note= "Homologous to heat shock protein, hsp60"
 FT Modified-site 103. .105
 FT /note= "N-Glycosylation site"
 FT Modified-site 144. .146
 FT /note= "N-Glycosylation site"
 FT Domain 154. .174
 FT /label= Zinc_finger_C2H2_type_domain
 FT Modified-site 191. .193
 FT /note= "N-Glycosylation site"
 FT Domain 196. .215
 FT /label= Zinc_finger_C2H2_type_domain
 FT Domain 219. .240
 FT /label= Zinc_finger_C2H2_type_domain
 FT Active-site 234. .238
 FT /label= Glutaredoxin_active_site
 FT Domain 329. .352
 FT /label= Zinc_finger_C2H2_type_domain
 FT Misc-difference 333
 FT /note= "Encoded by TTT"
 FT Domain 369. .391
 FT /label= Zinc_finger_C2H2_type_domain
 FT Modified-site 412. .414
 FT /note= "N-Glycosylation site"
 FT Modified-site 562. .564
 FT /note= "N-Glycosylation site"
 XX
 PN WO200027875-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-US026213.
 XX
 PR 06-NOV-1998; 98US-00187330.
 XX
 PA (USAS) GOVERNMENT US REPRESENT AS.
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX
 PI Gozes I, Brenneman DE, Bassan M, Zamostiano R;
 XX
 DR WPI; 2000-376491/32.
 DR N-PSDB; AAD00749.
 XX
 PT New nucleic acid encoding an activity dependent neurotrophic factor III
 PT (ADNF III) useful in the treatment of neurological deficiencies and for
 PT preventing neuronal cell death.
 XX
 PS Claim 12; Fig 12; 136pp; English.
 XX

CC The present sequence is the the human Activity Dependent Neurotrophic
 CC Factor III (ADNF III) H3 protein, also called an Activity Dependent
 CC Neuroprotective Protein (ADNP). The gene was mapped to chromosome 20q13.2
 CC and is linked to autosomal dominant nocturnal frontal-lobe epilepsy
 CC (ADNFLE) gene. It is expressed in the astrocytes, brain and also in
 CC foetal lung and endocrine tissues. This sequence has homology to ADNF I
 CC and hsp60, heat shock protein and PIF1, a DNA repair protein. The ADNF
 CC III polypeptides are useful for the treatment of neurological
 CC deficiencies and for prevention of neuronal cell death associated with
 CC gp120, the envelope protein from HIV; N-methyl-D-Aspartic acid (excito-
 CC toxicity); tetrodotoxin (blockage of electrical activity); and beta-
 CC amyloid peptide, a substance related to neuronal degeneration in
 CC Alzheimer's disease. It is useful for the treatment of Huntington's
 CC disease, AIDS dementia complex, epilepsy, neuropathic pain syndromes,
 CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), mitochondrial
 CC abnormalities, Leber's disease, Wernicke's encephalopathy, Alzheimer's
 CC disease, homocysteinuria, hyperprolinemia, sulphite oxide disease,
 CC Tourette's syndrome, oxidative stress induced neuronal death, Down's
 CC syndrome, developmental retardation and learning impairments, drug
 CC addiction, tolerance and dependency

XX

SQ Sequence 726 AA;

Query Match 100.0%; Score 41; DB 3; Length 726;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
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 Db 59 NAPVSIPQ 66

RESULT 49

AAW64695

ID AAW64695 standard; protein; 781 AA.

XX

AC AAW64695;

XX

DT 04-NOV-1998 (first entry)

XX

DE Mouse ADNF-III protein #2.

XX

KW Activity dependent neurotrophic factor III: ADNF-III; ADNP; cell death;

KW activity dependent neuroprotective protein; neurone; excito-toxicity;

KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;

KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;

KW HIV infection.

XX

OS Mus sp.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.

XX

PF 06-FEB-1998; 98WO-US002485.

XX

PR 07-FEB-1997; 97US-0037404P.

XX
PA (USSH) US SEC HEALTH & HUMAN SERVICES.
XX
PI Gozes I, Brenneman DE, Bassan M;
XX
DR WPI; 1998-447239/38.
XX
PT Activity dependent neurotrophic factor III polypeptide - useful
PT therapeutically to prevent neuronal cell death associated with e.g. HIV
PT infection, excito-toxicity or Alzheimer's disease.
XX
PS Disclosure; Fig 5c; 121pp; English.
XX
CC This sequence represents a mouse activity dependent neurotrophic factor
CC III, ADNF-III (also known as activity dependent neuroprotective protein,
CC ADNP). ADNF III polypeptides can be used to prevent neuronal cell death,
CC of e.g. the spinal cord, hippocampal, cerebral cortical or cholinergic
CC neurones associated with e.g. HIV infection, excito-toxicity induced by N
CC -methyl-D-aspartate stimulation or beta-amyloid peptide in Alzheimer's
CC disease. The polypeptides can also be combined with a carrier to
CC alleviate learning impairment produced by cholinergic blockage in
CC Alzheimer's patients. The nucleic acids are useful in polypeptide
CC production and to detect ADNF III polynucleotide in biological samples,
CC while the antibodies are useful therapeutically and to isolate ADNF III
CC polypeptides
XX
SQ Sequence 781 AA;

Query Match 100.0%; Score 41; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 33 NAPVSIPQ 40

RESULT 50

AAW64694

ID AAW64694 standard; protein; 787 AA.

XX

AC AAW64694;

XX

DT 04-NOV-1998 (first entry)

XX

DE Human ADNF-III protein #2.

XX

KW Activity dependent neurotrophic factor III; ADNF-III; ADNP; cell death;
KW activity dependent neuroprotective protein; neurone; excito-toxicity;
KW spinal cord; hippocampus; cerebral cortex; cholinergic; beta-amyloid;
KW N-methyl-D-aspartate; Alzheimer's disease; human immunodeficiency virus;
KW HIV infection.

XX

OS Homo sapiens.

XX

PN WO9835042-A2.

XX

PD 13-AUG-1998.
 XX
 PF 06-FEB-1998; 98WO-US002485.
 XX
 PR 07-FEB-1997; 97US-0037404P.
 XX
 PA (USSH) US SEC HEALTH & HUMAN SERVICES.
 XX
 PI Gozes I, Brenneman DE, Bassan M;
 XX
 DR WPI; 1998-447239/38.
 XX
 PT Activity dependent neurotrophic factor III polypeptide - useful
 PT therapeutically to prevent neuronal cell death associated with e.g. HIV
 PT infection, excito-toxicity or Alzheimer's disease.
 XX
 PS Disclosure; Fig 5c; 121pp; English.
 XX
 CC This sequence represents a human activity dependent neurotrophic factor
 CC type III, ADNF-III (also known as activity dependent neuroprotective
 CC protein, ADNP). ADNF III polypeptides can be used to prevent neuronal
 CC cell death, of e.g. the spinal cord, hippocampal, cerebral cortical or
 CC cholinergic neurones associated with e.g. HIV infection, excito-toxicity
 CC induced by N-methyl-D-aspartate stimulation or beta-amyloid peptide in
 CC Alzheimer's disease. The polypeptides can also be combined with a carrier
 CC to alleviate learning impairment produced by cholinergic blockage in
 CC Alzheimer's patients. The nucleic acids are useful in polypeptide
 CC production and to detect ADNF III polynucleotide in biological samples,
 CC while the antibodies are useful therapeutically and to isolate ADNF III
 CC polypeptides
 XX
 SQ Sequence 787 AA;

Query Match 100.0%; Score 41; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 33 NAPVSIPQ 40

Search completed: April 26, 2006, 00:18:29
 Job time : 231 secs

OM protein - protein search, using sw model

Run on: April 26, 2006, 00:23:58 ; Search time 26 Seconds
 (without alignments)
 13.539 Million cell updates/sec

Title: US-10-748-765-2
 Perfect score: 41
 Sequence: 1 NAPVSIPQ 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*
 1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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 8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	35	85.4	329	7	US-11-079-463-9097	Sequence 9097, Ap
2	35	85.4	808	7	US-11-110-082-38	Sequence 38, Appl
3	34	82.9	503	7	US-11-188-298-5829	Sequence 5829, Ap
4	34	82.9	503	7	US-11-188-298-9524	Sequence 9524, Ap
5	34	82.9	503	7	US-11-188-298-13806	Sequence 13806, A
6	34	82.9	512	7	US-11-188-298-17178	Sequence 17178, A
7	34	82.9	641	7	US-11-188-298-5631	Sequence 5631, Ap
8	33	80.5	574	6	US-10-821-234-1624	Sequence 1624, Ap
9	32	78.0	476	7	US-11-143-980-44	Sequence 44, Appl

10	32	78.0	513	7	US-11-096-568A-12983	Sequence 12983, A
11	32	78.0	548	7	US-11-096-568A-12982	Sequence 12982, A
12	32	78.0	613	7	US-11-096-568A-12981	Sequence 12981, A
13	31	75.6	358	6	US-10-467-657-6986	Sequence 6986, Ap
14	31	75.6	424	7	US-11-188-298-21875	Sequence 21875, A
15	31	75.6	481	6	US-10-506-454-1067	Sequence 1067, Ap
16	31	75.6	487	7	US-11-188-298-5842	Sequence 5842, Ap
17	31	75.6	505	7	US-11-188-298-15955	Sequence 15955, A
18	31	75.6	506	7	US-11-188-298-3808	Sequence 3808, Ap
19	31	75.6	511	7	US-11-188-298-14719	Sequence 14719, A
20	31	75.6	521	6	US-10-793-626-532	Sequence 532, App
21	30	73.2	18	7	US-11-068-783-39	Sequence 39, Appl
22	30	73.2	18	7	US-11-068-783-40	Sequence 40, Appl
23	30	73.2	239	7	US-11-153-071-12	Sequence 12, Appl
24	30	73.2	250	7	US-11-096-568A-3188	Sequence 3188, Ap
25	30	73.2	250	7	US-11-096-568A-3189	Sequence 3189, Ap
26	30	73.2	285	6	US-10-714-887-304	Sequence 304, App
27	30	73.2	322	7	US-11-052-554A-131	Sequence 131, App
28	30	73.2	339	7	US-11-188-298-10980	Sequence 10980, A
29	30	73.2	367	6	US-10-821-234-1569	Sequence 1569, Ap
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32	30	73.2	730	7	US-11-188-298-8921	Sequence 8921, Ap
33	30	73.2	784	7	US-11-087-099-3348	Sequence 3348, Ap
34	30	73.2	784	7	US-11-188-298-20082	Sequence 20082, A
35	30	73.2	829	6	US-10-649-591-16	Sequence 16, Appl
36	30	73.2	829	6	US-10-501-035-379	Sequence 379, App
37	30	73.2	829	7	US-11-090-739-122	Sequence 122, App
38	30	73.2	829	7	US-11-186-284-18	Sequence 18, Appl
39	30	73.2	829	7	US-11-200-822-1	Sequence 1, Appli
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41	30	73.2	868	7	US-11-188-298-12858	Sequence 12858, A
42	30	73.2	869	7	US-11-188-298-20296	Sequence 20296, A
43	30	73.2	927	7	US-11-096-568A-31020	Sequence 31020, A
44	30	73.2	946	7	US-11-207-626A-44	Sequence 44, Appl
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51	29	70.7	18	7	US-11-068-783-41	Sequence 41, Appl
52	29	70.7	370	7	US-11-188-298-3474	Sequence 3474, Ap
53	29	70.7	390	7	US-11-087-099-8409	Sequence 8409, Ap
54	29	70.7	449	6	US-10-487-466A-9	Sequence 9, Appli
55	29	70.7	463	7	US-11-188-298-2207	Sequence 2207, Ap
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61	29	70.7	573	7	US-11-188-298-11051	Sequence 11051, A
62	29	70.7	644	7	US-11-079-463-5855	Sequence 5855, Ap
63	29	70.7	761	6	US-10-204-639-19	Sequence 19, Appl
64	29	70.7	833	6	US-10-467-657-3876	Sequence 3876, Ap
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67	28	68.3	167	6	US-10-745-586-184	Sequence 184, App
68	28	68.3	180	7	US-11-096-568A-3993	Sequence 3993, Ap
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70	28	68.3	243	7	US-11-087-099-5965	Sequence 5965, Ap
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72	28	68.3	274	7	US-11-096-568A-3117	Sequence 3117, Ap
73	28	68.3	303	7	US-11-096-568A-3116	Sequence 3116, Ap
74	28	68.3	303	7	US-11-096-568A-3118	Sequence 3118, Ap
75	28	68.3	305	7	US-11-096-568A-7516	Sequence 7516, Ap
76	28	68.3	306	7	US-11-096-568A-3115	Sequence 3115, Ap
77	28	68.3	315	7	US-11-045-004-1894	Sequence 1894, Ap
78	28	68.3	332	7	US-11-079-463-9488	Sequence 9488, Ap
79	28	68.3	353	7	US-11-072-512-2052	Sequence 2052, Ap
80	28	68.3	374	6	US-10-513-269-5	Sequence 5, Appli
81	28	68.3	388	6	US-10-527-500-17	Sequence 17, Appl
82	28	68.3	398	7	US-11-130-391-1	Sequence 1, Appli
83	28	68.3	398	7	US-11-130-391-2	Sequence 2, Appli
84	28	68.3	398	7	US-11-129-574-1	Sequence 1, Appli
85	28	68.3	398	7	US-11-129-574-2	Sequence 2, Appli
86	28	68.3	399	7	US-11-188-298-15324	Sequence 15324, A
87	28	68.3	427	6	US-10-508-263-96	Sequence 96, Appl
88	28	68.3	431	7	US-11-087-099-4628	Sequence 4628, Ap
89	28	68.3	444	7	US-11-087-099-956	Sequence 956, App
90	28	68.3	444	7	US-11-188-298-11922	Sequence 11922, A
91	28	68.3	457	7	US-11-194-246-326	Sequence 326, App
92	28	68.3	471	7	US-11-079-463-9442	Sequence 9442, Ap
93	28	68.3	479	7	US-11-074-176-168	Sequence 168, App
94	28	68.3	483	7	US-11-188-298-12703	Sequence 12703, A
95	28	68.3	501	7	US-11-188-298-13662	Sequence 13662, A
96	28	68.3	503	7	US-11-188-298-3758	Sequence 3758, Ap
97	28	68.3	503	7	US-11-188-298-13768	Sequence 13768, A
98	28	68.3	503	7	US-11-188-298-22378	Sequence 22378, A
99	28	68.3	505	7	US-11-188-298-8716	Sequence 8716, Ap
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101	28	68.3	506	7	US-11-188-298-9019	Sequence 9019, Ap
102	28	68.3	506	7	US-11-188-298-9318	Sequence 9318, Ap
103	28	68.3	549	7	US-11-072-512-3526	Sequence 3526, Ap
104	28	68.3	566	7	US-11-188-298-3470	Sequence 3470, Ap
105	28	68.3	592	7	US-11-188-298-7356	Sequence 7356, Ap
106	28	68.3	592	7	US-11-188-298-14829	Sequence 14829, A
107	28	68.3	598	7	US-11-188-298-1943	Sequence 1943, Ap
108	28	68.3	637	7	US-11-188-298-12194	Sequence 12194, A
109	28	68.3	750	7	US-11-188-298-9536	Sequence 9536, Ap
110	28	68.3	805	6	US-10-467-657-1930	Sequence 1930, Ap
111	28	68.3	882	6	US-10-194-487-574	Sequence 574, App
112	28	68.3	882	6	US-10-195-883-574	Sequence 574, App
113	28	68.3	882	6	US-10-195-888-574	Sequence 574, App
114	28	68.3	882	6	US-10-195-889-574	Sequence 574, App
115	28	68.3	2760	7	US-11-124-367A-444	Sequence 444, App
116	28	68.3	2803	7	US-11-124-367A-442	Sequence 442, App
117	28	68.3	2803	7	US-11-124-367A-445	Sequence 445, App
118	28	68.3	2984	7	US-11-124-367A-443	Sequence 443, App
119	28	68.3	3027	7	US-11-124-367A-441	Sequence 441, App
120	28	68.3	3300	7	US-11-052-554A-133	Sequence 133, App
121	27	65.9	50	5	US-09-978-360A-624	Sequence 624, App
122	27	65.9	57	6	US-10-467-657-728	Sequence 728, App
123	27	65.9	92	7	US-11-212-443-36	Sequence 36, Appl

124	27	65.9	103	7	US-11-212-443-38	Sequence 38, Appl
125	27	65.9	113	6	US-10-793-626-2338	Sequence 2338, Ap
126	27	65.9	113	7	US-11-096-568A-152	Sequence 152, App
127	27	65.9	113	7	US-11-096-568A-153	Sequence 153, App
128	27	65.9	134	7	US-11-096-568A-14850	Sequence 14850, A
129	27	65.9	154	6	US-10-467-657-2034	Sequence 2034, Ap
130	27	65.9	155	7	US-11-096-568A-9749	Sequence 9749, Ap
131	27	65.9	163	7	US-11-188-298-7934	Sequence 7934, Ap
132	27	65.9	177	7	US-11-194-246-416	Sequence 416, App
133	27	65.9	196	7	US-11-172-740-2521	Sequence 2521, Ap
134	27	65.9	196	7	US-11-172-740-2522	Sequence 2522, Ap
135	27	65.9	196	7	US-11-188-298-1745	Sequence 1745, Ap
136	27	65.9	197	7	US-11-172-740-2520	Sequence 2520, Ap
137	27	65.9	206	7	US-11-123-241-131	Sequence 131, App
138	27	65.9	216	7	US-11-079-463-5974	Sequence 5974, Ap
139	27	65.9	225	7	US-11-229-769-238	Sequence 238, App
140	27	65.9	225	7	US-11-229-769-353	Sequence 353, App
141	27	65.9	266	7	US-11-096-568A-19487	Sequence 19487, A
142	27	65.9	266	7	US-11-045-004-662	Sequence 662, App
143	27	65.9	270	6	US-10-714-887-388	Sequence 388, App
144	27	65.9	280	6	US-10-979-095-10	Sequence 10, Appl
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146	27	65.9	301	7	US-11-087-099-434	Sequence 434, App
147	27	65.9	306	7	US-11-087-099-1143	Sequence 1143, Ap
148	27	65.9	310	7	US-11-087-099-2317	Sequence 2317, Ap
149	27	65.9	315	7	US-11-096-568A-19486	Sequence 19486, A
150	27	65.9	362	7	US-11-188-298-13847	Sequence 13847, A
151	27	65.9	388	6	US-10-527-500-61	Sequence 61, Appl
152	27	65.9	391	7	US-11-087-099-6482	Sequence 6482, Ap
153	27	65.9	391	7	US-11-087-099-10113	Sequence 10113, A
154	27	65.9	405	7	US-11-188-298-15624	Sequence 15624, A
155	27	65.9	414	7	US-11-087-099-6506	Sequence 6506, Ap
156	27	65.9	415	6	US-10-523-588-14	Sequence 14, Appl
157	27	65.9	415	6	US-10-523-588-15	Sequence 15, Appl
158	27	65.9	434	7	US-11-268-629-7	Sequence 7, Appli
159	27	65.9	434	7	US-11-188-298-11425	Sequence 11425, A
160	27	65.9	439	7	US-11-045-004-314	Sequence 314, App
161	27	65.9	442	7	US-11-188-298-5678	Sequence 5678, Ap
162	27	65.9	446	7	US-11-096-568A-34276	Sequence 34276, A
163	27	65.9	447	6	US-10-523-588-16	Sequence 16, Appl
164	27	65.9	449	7	US-11-096-568A-34275	Sequence 34275, A
165	27	65.9	467	7	US-11-096-568A-34274	Sequence 34274, A
166	27	65.9	488	7	US-11-188-298-1585	Sequence 1585, Ap
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174	27	65.9	506	7	US-11-188-298-15225	Sequence 15225, A
175	27	65.9	507	7	US-11-096-568A-6960	Sequence 6960, Ap
176	27	65.9	512	7	US-11-079-463-6040	Sequence 6040, Ap
177	27	65.9	515	7	US-11-096-568A-6959	Sequence 6959, Ap
178	27	65.9	517	7	US-11-096-568A-6958	Sequence 6958, Ap
179	27	65.9	554	7	US-11-229-769-352	Sequence 352, App
180	27	65.9	556	7	US-11-154-227-98	Sequence 98, Appl

181	27	65.9	582	7	US-11-205-109-36	Sequence 36, Appl
182	27	65.9	599	7	US-11-188-298-11959	Sequence 11959, A
183	27	65.9	659	7	US-11-079-463-6605	Sequence 6605, Ap
184	27	65.9	689	6	US-10-469-469-191	Sequence 191, App
185	27	65.9	691	6	US-10-330-773-485	Sequence 485, App
186	27	65.9	716	7	US-11-188-298-18748	Sequence 18748, A
187	27	65.9	747	6	US-10-501-035-224	Sequence 224, App
188	27	65.9	756	7	US-11-045-004-2637	Sequence 2637, Ap
189	27	65.9	762	7	US-11-188-298-11787	Sequence 11787, A
190	27	65.9	769	7	US-11-087-099-4321	Sequence 4321, Ap
191	27	65.9	769	7	US-11-188-298-14999	Sequence 14999, A
192	27	65.9	804	6	US-10-453-372-650	Sequence 650, App
193	27	65.9	821	7	US-11-188-298-3487	Sequence 3487, Ap
194	27	65.9	825	6	US-10-453-372-644	Sequence 644, App
195	27	65.9	837	7	US-11-052-554A-159	Sequence 159, App
196	27	65.9	865	7	US-11-109-156-4	Sequence 4, Appli
197	27	65.9	1250	6	US-10-531-036-37	Sequence 37, Appl
198	27	65.9	1582	7	US-11-045-004-12	Sequence 12, Appl
199	27	65.9	2442	6	US-10-469-469-252	Sequence 252, App
200	26.5	64.6	274	6	US-10-467-657-706	Sequence 706, App
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202	26	63.4	68	7	US-11-172-193-3	Sequence 3, Appli
203	26	63.4	85	5	US-09-978-360A-601	Sequence 601, App
204	26	63.4	85	5	US-09-978-360A-602	Sequence 602, App
205	26	63.4	85	5	US-09-978-360A-779	Sequence 779, App
206	26	63.4	85	6	US-10-745-586-85	Sequence 85, Appl
207	26	63.4	85	6	US-10-194-487-460	Sequence 460, App
208	26	63.4	85	6	US-10-195-883-460	Sequence 460, App
209	26	63.4	85	6	US-10-195-888-460	Sequence 460, App
210	26	63.4	85	6	US-10-195-889-460	Sequence 460, App
211	26	63.4	85	6	US-10-218-784-112	Sequence 112, App
212	26	63.4	85	6	US-10-219-061-112	Sequence 112, App
213	26	63.4	85	6	US-10-219-062-112	Sequence 112, App
214	26	63.4	85	6	US-10-219-064-112	Sequence 112, App
215	26	63.4	85	6	US-10-233-134-112	Sequence 112, App
216	26	63.4	85	7	US-11-172-193-2	Sequence 2, Appli
217	26	63.4	96	6	US-10-467-657-8984	Sequence 8984, Ap
218	26	63.4	103	7	US-11-079-463-5580	Sequence 5580, Ap
219	26	63.4	131	7	US-11-188-298-5610	Sequence 5610, Ap
220	26	63.4	132	7	US-11-188-298-16074	Sequence 16074, A
221	26	63.4	138	7	US-11-072-512-3328	Sequence 3328, Ap
222	26	63.4	147	7	US-11-096-568A-11815	Sequence 11815, A
223	26	63.4	149	7	US-11-096-568A-25620	Sequence 25620, A
224	26	63.4	149	7	US-11-188-298-620	Sequence 620, App
225	26	63.4	155	7	US-11-096-568A-24177	Sequence 24177, A
226	26	63.4	157	7	US-11-096-568A-4245	Sequence 4245, Ap
227	26	63.4	157	7	US-11-096-568A-11814	Sequence 11814, A
228	26	63.4	172	7	US-11-096-568A-21275	Sequence 21275, A
229	26	63.4	174	7	US-11-096-568A-24176	Sequence 24176, A
230	26	63.4	188	7	US-11-096-568A-4244	Sequence 4244, Ap
231	26	63.4	188	7	US-11-096-568A-4738	Sequence 4738, Ap
232	26	63.4	192	7	US-11-072-175-193	Sequence 193, App
233	26	63.4	195	7	US-11-096-568A-4737	Sequence 4737, Ap
234	26	63.4	196	7	US-11-172-740-2519	Sequence 2519, Ap
235	26	63.4	196	7	US-11-172-740-2523	Sequence 2523, Ap
236	26	63.4	196	7	US-11-188-298-9778	Sequence 9778, Ap
237	26	63.4	197	7	US-11-098-686-10982	Sequence 10982, A

238	26	63.4	197	7	US-11-087-099-7517	Sequence 7517, Ap
239	26	63.4	197	7	US-11-087-099-10741	Sequence 10741, A
240	26	63.4	197	7	US-11-172-740-584	Sequence 584, App
241	26	63.4	197	7	US-11-172-740-2516	Sequence 2516, Ap
242	26	63.4	197	7	US-11-172-740-2517	Sequence 2517, Ap
243	26	63.4	197	7	US-11-188-298-9925	Sequence 9925, Ap
244	26	63.4	197	7	US-11-188-298-10773	Sequence 10773, A
245	26	63.4	197	7	US-11-188-298-15641	Sequence 15641, A
246	26	63.4	197	7	US-11-188-298-16376	Sequence 16376, A
247	26	63.4	197	7	US-11-188-298-17984	Sequence 17984, A
248	26	63.4	197	7	US-11-188-298-21565	Sequence 21565, A
249	26	63.4	200	6	US-10-878-556A-64	Sequence 64, Appl
250	26	63.4	200	7	US-11-069-642-131	Sequence 131, App
251	26	63.4	200	7	US-11-079-463-8717	Sequence 8717, Ap
252	26	63.4	201	7	US-11-096-568A-4243	Sequence 4243, Ap
253	26	63.4	204	7	US-11-096-568A-21453	Sequence 21453, A
254	26	63.4	205	7	US-11-096-568A-4736	Sequence 4736, Ap
255	26	63.4	206	7	US-11-015-546A-7	Sequence 7, Appli
256	26	63.4	212	6	US-10-980-388-84	Sequence 84, Appl
257	26	63.4	212	7	US-11-015-546A-5	Sequence 5, Appli
258	26	63.4	216	7	US-11-096-568A-21452	Sequence 21452, A
259	26	63.4	219	7	US-11-015-546A-4	Sequence 4, Appli
260	26	63.4	219	7	US-11-098-686-10314	Sequence 10314, A
261	26	63.4	227	7	US-11-087-099-6569	Sequence 6569, Ap
262	26	63.4	227	7	US-11-096-568A-18799	Sequence 18799, A
263	26	63.4	236	7	US-11-104-111-13	Sequence 13, Appl
264	26	63.4	238	7	US-11-087-099-9752	Sequence 9752, Ap
265	26	63.4	239	7	US-11-096-568A-30962	Sequence 30962, A
266	26	63.4	240	7	US-11-096-568A-18798	Sequence 18798, A
267	26	63.4	243	7	US-11-096-568A-33445	Sequence 33445, A
268	26	63.4	245	7	US-11-188-298-21931	Sequence 21931, A
269	26	63.4	248	7	US-11-188-298-17613	Sequence 17613, A
270	26	63.4	253	7	US-11-015-546A-2	Sequence 2, Appli
271	26	63.4	254	6	US-10-986-405-250	Sequence 250, App
272	26	63.4	255	7	US-11-087-099-7661	Sequence 7661, Ap
273	26	63.4	261	7	US-11-096-568A-7079	Sequence 7079, Ap
274	26	63.4	267	7	US-11-096-568A-17262	Sequence 17262, A
275	26	63.4	269	7	US-11-015-546A-10	Sequence 10, Appl
276	26	63.4	269	7	US-11-096-568A-17261	Sequence 17261, A
277	26	63.4	273	6	US-10-495-597-8	Sequence 8, Appli
278	26	63.4	274	7	US-11-015-546A-12	Sequence 12, Appl
279	26	63.4	274	7	US-11-098-686-11273	Sequence 11273, A
280	26	63.4	275	7	US-11-096-568A-17260	Sequence 17260, A
281	26	63.4	276	7	US-11-096-568A-12522	Sequence 12522, A
282	26	63.4	287	7	US-11-096-568A-2937	Sequence 2937, Ap
283	26	63.4	288	7	US-11-087-099-10942	Sequence 10942, A
284	26	63.4	289	6	US-10-793-626-3254	Sequence 3254, Ap
285	26	63.4	291	7	US-11-096-568A-21274	Sequence 21274, A
286	26	63.4	292	7	US-11-172-740-389	Sequence 389, App
287	26	63.4	292	7	US-11-172-740-390	Sequence 390, App
288	26	63.4	299	6	US-10-858-730-17	Sequence 17, Appl
289	26	63.4	307	6	US-10-508-263-113	Sequence 113, App
290	26	63.4	317	7	US-11-096-568A-12521	Sequence 12521, A
291	26	63.4	318	7	US-11-096-568A-30961	Sequence 30961, A
292	26	63.4	321	7	US-11-024-959-333	Sequence 333, App
293	26	63.4	324	7	US-11-096-568A-18885	Sequence 18885, A
294	26	63.4	335	7	US-11-096-568A-30960	Sequence 30960, A

295	26	63.4	346	7	US-11-188-298-5158	Sequence 5158, Ap
296	26	63.4	359	6	US-10-513-269-3	Sequence 3, Appli
297	26	63.4	367	7	US-11-188-298-5264	Sequence 5264, Ap
298	26	63.4	369	7	US-11-087-099-2498	Sequence 2498, Ap
299	26	63.4	369	7	US-11-188-298-16484	Sequence 16484, A
300	26	63.4	369	7	US-11-188-298-19804	Sequence 19804, A
301	26	63.4	371	7	US-11-087-099-4683	Sequence 4683, Ap
302	26	63.4	379	6	US-10-793-626-2810	Sequence 2810, Ap
303	26	63.4	379	6	US-10-530-240-2	Sequence 2, Appli
304	26	63.4	379	7	US-11-052-554A-193	Sequence 193, App
305	26	63.4	391	7	US-11-087-099-4105	Sequence 4105, Ap
306	26	63.4	392	7	US-11-087-099-9567	Sequence 9567, Ap
307	26	63.4	393	6	US-10-506-454-1271	Sequence 1271, Ap
308	26	63.4	399	7	US-11-087-099-512	Sequence 512, App
309	26	63.4	405	7	US-11-096-568A-1768	Sequence 1768, Ap
310	26	63.4	406	7	US-11-096-568A-1767	Sequence 1767, Ap
311	26	63.4	408	7	US-11-087-099-1741	Sequence 1741, Ap
312	26	63.4	408	7	US-11-087-099-3610	Sequence 3610, Ap
313	26	63.4	409	7	US-11-188-298-11877	Sequence 11877, A
314	26	63.4	413	7	US-11-188-298-14323	Sequence 14323, A
315	26	63.4	422	7	US-11-096-568A-23955	Sequence 23955, A
316	26	63.4	425	7	US-11-096-568A-1766	Sequence 1766, Ap
317	26	63.4	427	7	US-11-188-298-759	Sequence 759, App
318	26	63.4	428	7	US-11-087-099-4644	Sequence 4644, Ap
319	26	63.4	428	7	US-11-188-298-363	Sequence 363, App
320	26	63.4	441	7	US-11-188-298-13240	Sequence 13240, A
321	26	63.4	441	7	US-11-188-298-17621	Sequence 17621, A
322	26	63.4	443	7	US-11-188-298-1413	Sequence 1413, Ap
323	26	63.4	448	6	US-10-618-320A-25	Sequence 25, Appl
324	26	63.4	448	7	US-11-188-298-20754	Sequence 20754, A
325	26	63.4	449	7	US-11-096-568A-7359	Sequence 7359, Ap
326	26	63.4	450	6	US-10-714-995-6	Sequence 6, Appli
327	26	63.4	450	7	US-11-188-298-18427	Sequence 18427, A
328	26	63.4	452	7	US-11-096-568A-9903	Sequence 9903, Ap
329	26	63.4	455	7	US-11-096-568A-7358	Sequence 7358, Ap
330	26	63.4	458	6	US-10-194-487-496	Sequence 496, App
331	26	63.4	458	6	US-10-195-883-496	Sequence 496, App
332	26	63.4	458	6	US-10-195-888-496	Sequence 496, App
333	26	63.4	458	6	US-10-195-889-496	Sequence 496, App
334	26	63.4	461	7	US-11-188-298-4696	Sequence 4696, Ap
335	26	63.4	462	7	US-11-096-568A-14622	Sequence 14622, A
336	26	63.4	464	7	US-11-096-568A-25263	Sequence 25263, A
337	26	63.4	465	7	US-11-096-568A-9902	Sequence 9902, Ap
338	26	63.4	466	7	US-11-096-568A-7357	Sequence 7357, Ap
339	26	63.4	468	7	US-11-072-512-3664	Sequence 3664, Ap
340	26	63.4	470	7	US-11-096-568A-14621	Sequence 14621, A
341	26	63.4	472	7	US-11-096-568A-25262	Sequence 25262, A
342	26	63.4	476	7	US-11-087-099-8363	Sequence 8363, Ap
343	26	63.4	476	7	US-11-188-298-11495	Sequence 11495, A
344	26	63.4	477	7	US-11-188-298-5640	Sequence 5640, Ap
345	26	63.4	478	7	US-11-188-298-18308	Sequence 18308, A
346	26	63.4	479	7	US-11-188-298-13224	Sequence 13224, A
347	26	63.4	482	7	US-11-188-298-5443	Sequence 5443, Ap
348	26	63.4	483	7	US-11-087-099-4915	Sequence 4915, Ap
349	26	63.4	483	7	US-11-087-099-5880	Sequence 5880, Ap
350	26	63.4	483	7	US-11-188-298-6092	Sequence 6092, Ap
351	26	63.4	483	7	US-11-188-298-20426	Sequence 20426, A

352	26	63.4	487	7	US-11-188-298-14966	Sequence 14966, A
353	26	63.4	488	7	US-11-188-298-6414	Sequence 6414, Ap
354	26	63.4	490	7	US-11-072-512-3841	Sequence 3841, Ap
355	26	63.4	492	7	US-11-188-298-740	Sequence 740, App
356	26	63.4	493	7	US-11-188-298-19143	Sequence 19143, A
357	26	63.4	497	7	US-11-188-298-6557	Sequence 6557, Ap
358	26	63.4	498	7	US-11-079-463-10405	Sequence 10405, A
359	26	63.4	508	6	US-10-514-534-7	Sequence 7, Appli
360	26	63.4	508	7	US-11-093-274-41	Sequence 41, Appl
361	26	63.4	508	7	US-11-188-298-4306	Sequence 4306, Ap
362	26	63.4	508	7	US-11-188-298-18082	Sequence 18082, A
363	26	63.4	513	7	US-11-087-099-11316	Sequence 11316, A
364	26	63.4	513	7	US-11-087-099-11916	Sequence 11916, A
365	26	63.4	513	7	US-11-096-568A-14620	Sequence 14620, A
366	26	63.4	514	7	US-11-188-298-18211	Sequence 18211, A
367	26	63.4	515	7	US-11-096-568A-25261	Sequence 25261, A
368	26	63.4	516	7	US-11-087-099-5425	Sequence 5425, Ap
369	26	63.4	517	7	US-11-096-568A-9901	Sequence 9901, Ap
370	26	63.4	521	7	US-11-087-099-5589	Sequence 5589, Ap
371	26	63.4	521	7	US-11-188-298-5101	Sequence 5101, Ap
372	26	63.4	523	7	US-11-087-099-1192	Sequence 1192, Ap
373	26	63.4	523	7	US-11-087-099-8662	Sequence 8662, Ap
374	26	63.4	523	7	US-11-188-298-8049	Sequence 8049, Ap
375	26	63.4	523	7	US-11-188-298-12140	Sequence 12140, A
376	26	63.4	532	7	US-11-087-099-12403	Sequence 12403, A
377	26	63.4	533	7	US-11-124-368A-335	Sequence 335, App
378	26	63.4	540	7	US-11-099-691-2	Sequence 2, Appli
379	26	63.4	565	6	US-10-506-454-531	Sequence 531, App
380	26	63.4	573	7	US-11-087-099-9871	Sequence 9871, Ap
381	26	63.4	573	7	US-11-188-298-9121	Sequence 9121, Ap
382	26	63.4	574	6	US-10-330-773-488	Sequence 488, App
383	26	63.4	611	7	US-11-188-298-5827	Sequence 5827, Ap
384	26	63.4	628	7	US-11-074-176-244	Sequence 244, App
385	26	63.4	635	6	US-10-055-877-67	Sequence 67, Appl
386	26	63.4	640	7	US-11-188-298-11801	Sequence 11801, A
387	26	63.4	642	6	US-10-995-561-631	Sequence 631, App
388	26	63.4	657	6	US-10-995-561-622	Sequence 622, App
389	26	63.4	657	7	US-11-193-561-27	Sequence 27, Appl
390	26	63.4	657	7	US-11-193-771-27	Sequence 27, Appl
391	26	63.4	657	7	US-11-193-789-27	Sequence 27, Appl
392	26	63.4	657	7	US-11-193-806-27	Sequence 27, Appl
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394	26	63.4	662	7	US-11-188-298-14498	Sequence 14498, A
395	26	63.4	668	6	US-10-467-657-5042	Sequence 5042, Ap
396	26	63.4	689	7	US-11-024-959-510	Sequence 510, App
397	26	63.4	701	6	US-10-055-877-65	Sequence 65, Appl
398	26	63.4	701	7	US-11-188-298-14136	Sequence 14136, A
399	26	63.4	723	7	US-11-087-099-5391	Sequence 5391, Ap
400	26	63.4	723	7	US-11-087-099-10818	Sequence 10818, A
401	26	63.4	723	7	US-11-188-298-4924	Sequence 4924, Ap
402	26	63.4	723	7	US-11-188-298-9986	Sequence 9986, Ap
403	26	63.4	740	7	US-11-110-837-2	Sequence 2, Appli
404	26	63.4	740	7	US-11-110-837-4	Sequence 4, Appli
405	26	63.4	742	7	US-11-087-099-7459	Sequence 7459, Ap
406	26	63.4	742	7	US-11-188-298-6837	Sequence 6837, Ap
407	26	63.4	745	7	US-11-147-109-8	Sequence 8, Appli
408	26	63.4	759	7	US-11-188-298-6146	Sequence 6146, Ap

409	26	63.4	762	7	US-11-188-298-13851	Sequence 13851, A
410	26	63.4	770	6	US-10-821-234-1269	Sequence 1269, Ap
411	26	63.4	770	7	US-11-087-099-7757	Sequence 7757, Ap
412	26	63.4	770	7	US-11-188-298-18193	Sequence 18193, A
413	26	63.4	782	6	US-10-793-626-2352	Sequence 2352, Ap
414	26	63.4	784	7	US-11-147-109-4	Sequence 4, Appli
415	26	63.4	793	7	US-11-024-959-368	Sequence 368, App
416	26	63.4	875	7	US-11-188-298-8045	Sequence 8045, Ap
417	26	63.4	879	6	US-10-204-639-58	Sequence 58, Appl
418	26	63.4	885	6	US-10-055-877-240	Sequence 240, App
419	26	63.4	885	6	US-10-055-877-241	Sequence 241, App
420	26	63.4	885	7	US-11-188-298-13076	Sequence 13076, A
421	26	63.4	901	7	US-11-087-099-1818	Sequence 1818, Ap
422	26	63.4	974	6	US-10-531-036-35	Sequence 35, Appl
423	26	63.4	1008	7	US-11-055-822-312	Sequence 312, App
424	26	63.4	1022	7	US-11-186-284-163	Sequence 163, App
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426	26	63.4	1025	7	US-11-188-298-21705	Sequence 21705, A
427	26	63.4	1049	6	US-10-131-826A-358	Sequence 358, App
428	26	63.4	1049	6	US-10-973-115B-358	Sequence 358, App
429	26	63.4	1049	6	US-10-216-161A-496	Sequence 496, App
430	26	63.4	1049	7	US-11-290-153-358	Sequence 358, App
431	26	63.4	1089	7	US-11-188-298-8351	Sequence 8351, Ap
432	26	63.4	1152	7	US-11-055-822-308	Sequence 308, App
433	26	63.4	1244	7	US-11-181-330-4	Sequence 4, Appli
434	26	63.4	1258	7	US-11-121-438-16	Sequence 16, Appl
435	26	63.4	1273	7	US-11-181-330-8	Sequence 8, Appli
436	26	63.4	1432	6	US-10-510-386-218	Sequence 218, App
437	26	63.4	1449	7	US-11-052-554A-237	Sequence 237, App
438	26	63.4	1468	6	US-10-467-657-1088	Sequence 1088, Ap
439	26	63.4	1519	7	US-11-182-016-5	Sequence 5, Appli
440	26	63.4	1653	6	US-10-204-639-25	Sequence 25, Appl
441	26	63.4	1730	7	US-11-182-016-19	Sequence 19, Appl
442	26	63.4	1733	7	US-11-182-016-21	Sequence 21, Appl
443	26	63.4	1980	6	US-10-961-231-3	Sequence 3, Appli
444	26	63.4	1980	7	US-11-179-624-3	Sequence 3, Appli
445	26	63.4	2204	7	US-11-052-554A-134	Sequence 134, App
446	26	63.4	2410	7	US-11-175-689-8	Sequence 8, Appli
447	26	63.4	2591	6	US-10-453-372-718	Sequence 718, App
448	26	63.4	2602	6	US-10-453-372-716	Sequence 716, App
449	26	63.4	2602	6	US-10-937-658-5	Sequence 5, Appli
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451	26	63.4	2617	6	US-10-453-372-732	Sequence 732, App
452	26	63.4	2617	6	US-10-453-372-734	Sequence 734, App
453	26	63.4	2617	6	US-10-453-372-736	Sequence 736, App
454	26	63.4	2617	6	US-10-453-372-738	Sequence 738, App
455	26	63.4	2617	6	US-10-453-372-740	Sequence 740, App
456	26	63.4	2617	6	US-10-453-372-742	Sequence 742, App
457	26	63.4	2617	6	US-10-453-372-744	Sequence 744, App
458	26	63.4	2617	6	US-10-453-372-746	Sequence 746, App
459	26	63.4	2617	6	US-10-453-372-748	Sequence 748, App
460	26	63.4	2617	6	US-10-453-372-750	Sequence 750, App
461	26	63.4	2657	6	US-10-821-234-1262	Sequence 1262, Ap
462	26	63.4	3389	6	US-10-204-252-10	Sequence 10, Appl
463	26	63.4	3391	6	US-10-204-252-6	Sequence 6, Appli
464	26	63.4	3391	6	US-10-204-252-8	Sequence 8, Appli
465	26	63.4	3391	6	US-10-204-252-12	Sequence 12, Appl

466	26	63.4	3391	6	US-10-204-252-14	Sequence 14, Appl
467	26	63.4	3391	6	US-10-204-252-16	Sequence 16, Appl
468	26	63.4	3391	6	US-10-204-252-28	Sequence 28, Appl
469	26	63.4	3402	6	US-10-204-252-18	Sequence 18, Appl
470	26	63.4	3685	7	US-11-055-497A-8	Sequence 8, Appli
471	26	63.4	14130	7	US-11-175-689-9	Sequence 9, Appli
472	26	63.4	16990	7	US-11-175-689-7	Sequence 7, Appli
473	25	61.0	21	6	US-10-487-466A-3	Sequence 3, Appli
474	25	61.0	39	6	US-10-986-501-352	Sequence 352, App
475	25	61.0	51	6	US-10-512-340-41	Sequence 41, Appl
476	25	61.0	72	7	US-11-079-463-9060	Sequence 9060, Ap
477	25	61.0	76	7	US-11-096-568A-17010	Sequence 17010, A
478	25	61.0	85	7	US-11-096-568A-13428	Sequence 13428, A
479	25	61.0	91	6	US-10-485-788A-722	Sequence 722, App
480	25	61.0	91	7	US-11-053-076-92	Sequence 92, Appl
481	25	61.0	92	7	US-11-096-568A-13427	Sequence 13427, A
482	25	61.0	94	7	US-11-096-568A-13426	Sequence 13426, A
483	25	61.0	95	7	US-11-079-463-5808	Sequence 5808, Ap
484	25	61.0	96	6	US-10-467-657-4750	Sequence 4750, Ap
485	25	61.0	100	7	US-11-072-512-3175	Sequence 3175, Ap
486	25	61.0	103	7	US-11-096-568A-17008	Sequence 17008, A
487	25	61.0	105	7	US-11-072-512-2874	Sequence 2874, Ap
488	25	61.0	106	6	US-10-793-626-178	Sequence 178, App
489	25	61.0	106	6	US-10-793-626-1566	Sequence 1566, Ap
490	25	61.0	111	7	US-11-184-005-5	Sequence 5, Appli
491	25	61.0	111	7	US-11-072-512-2298	Sequence 2298, Ap
492	25	61.0	119	6	US-10-763-712A-59	Sequence 59, Appl
493	25	61.0	121	7	US-11-098-686-10834	Sequence 10834, A
494	25	61.0	127	7	US-11-210-756-19	Sequence 19, Appl
495	25	61.0	128	7	US-11-079-463-10086	Sequence 10086, A
496	25	61.0	130	7	US-11-087-099-2125	Sequence 2125, Ap
497	25	61.0	142	6	US-10-506-454-1093	Sequence 1093, Ap
498	25	61.0	143	7	US-11-096-568A-17665	Sequence 17665, A
499	25	61.0	148	6	US-10-510-386-120	Sequence 120, App
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505	25	61.0	158	7	US-11-072-512-3035	Sequence 3035, Ap
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507	25	61.0	159	7	US-11-096-568A-1406	Sequence 1406, Ap
508	25	61.0	160	7	US-11-096-568A-17664	Sequence 17664, A
509	25	61.0	160	7	US-11-188-298-8822	Sequence 8822, Ap
510	25	61.0	160	7	US-11-188-298-20803	Sequence 20803, A
511	25	61.0	163	6	US-10-506-454-823	Sequence 823, App
512	25	61.0	164	6	US-10-469-469-58	Sequence 58, Appl
513	25	61.0	168	7	US-11-087-099-12074	Sequence 12074, A
514	25	61.0	174	7	US-11-072-512-2183	Sequence 2183, Ap
515	25	61.0	179	7	US-11-188-298-16156	Sequence 16156, A
516	25	61.0	179	7	US-11-188-298-21720	Sequence 21720, A
517	25	61.0	181	7	US-11-188-298-5394	Sequence 5394, Ap
518	25	61.0	184	6	US-10-821-234-1415	Sequence 1415, Ap
519	25	61.0	188	6	US-10-980-388-101	Sequence 101, App
520	25	61.0	189	7	US-11-045-004-54	Sequence 54, Appl
521	25	61.0	193	7	US-11-079-463-7082	Sequence 7082, Ap
522	25	61.0	195	7	US-11-188-298-16989	Sequence 16989, A

523	25	61.0	197	6	US-10-915-002-259	Sequence 259, App
524	25	61.0	202	7	US-11-096-568A-7116	Sequence 7116, Ap
525	25	61.0	203	7	US-11-082-389-160	Sequence 160, App
526	25	61.0	206	6	US-10-467-657-5870	Sequence 5870, Ap
527	25	61.0	206	7	US-11-096-568A-7093	Sequence 7093, Ap
528	25	61.0	206	7	US-11-188-298-1850	Sequence 1850, Ap
529	25	61.0	207	7	US-11-124-367A-438	Sequence 438, App
530	25	61.0	207	7	US-11-188-298-16574	Sequence 16574, A
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534	25	61.0	221	7	US-11-080-628-2	Sequence 2, Appli
535	25	61.0	225	7	US-11-096-568A-1644	Sequence 1644, Ap
536	25	61.0	227	7	US-11-037-243-84	Sequence 84, Appl
537	25	61.0	231	6	US-10-506-454-1199	Sequence 1199, Ap
538	25	61.0	234	6	US-10-454-437-432	Sequence 432, App
539	25	61.0	237	7	US-11-188-298-7529	Sequence 7529, Ap
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541	25	61.0	241	7	US-11-188-298-19964	Sequence 19964, A
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543	25	61.0	243	7	US-11-188-298-15509	Sequence 15509, A
544	25	61.0	244	7	US-11-188-298-5931	Sequence 5931, Ap
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546	25	61.0	245	7	US-11-188-298-12717	Sequence 12717, A
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551	25	61.0	260	7	US-11-096-568A-7091	Sequence 7091, Ap
552	25	61.0	265	7	US-11-098-686-11404	Sequence 11404, A
553	25	61.0	265	7	US-11-096-568A-3046	Sequence 3046, Ap
554	25	61.0	266	7	US-11-087-099-9013	Sequence 9013, Ap
555	25	61.0	274	6	US-10-883-512-108	Sequence 108, App
556	25	61.0	274	7	US-11-087-099-2499	Sequence 2499, Ap
557	25	61.0	274	7	US-11-172-740-60	Sequence 60, Appl
558	25	61.0	275	7	US-11-096-568A-10458	Sequence 10458, A
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561	25	61.0	281	7	US-11-087-099-9922	Sequence 9922, Ap
562	25	61.0	281	7	US-11-172-740-61	Sequence 61, Appl
563	25	61.0	283	7	US-11-172-740-1727	Sequence 1727, Ap
564	25	61.0	286	7	US-11-098-686-10427	Sequence 10427, A
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571	25	61.0	302	7	US-11-124-367A-435	Sequence 435, App
572	25	61.0	304	7	US-11-096-568A-3358	Sequence 3358, Ap
573	25	61.0	306	7	US-11-096-568A-26369	Sequence 26369, A
574	25	61.0	307	7	US-11-096-568A-9693	Sequence 9693, Ap
575	25	61.0	308	6	US-10-467-657-1350	Sequence 1350, Ap
576	25	61.0	310	7	US-11-087-099-11679	Sequence 11679, A
577	25	61.0	311	7	US-11-045-004-606	Sequence 606, App
578	25	61.0	313	7	US-11-096-568A-10457	Sequence 10457, A
579	25	61.0	314	7	US-11-096-568A-3357	Sequence 3357, Ap

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581	25	61.0	314	7	US-11-188-298-21641	Sequence 21641, A
582	25	61.0	315	7	US-11-018-868-143	Sequence 143, App
583	25	61.0	317	6	US-10-995-561-798	Sequence 798, App
584	25	61.0	317	7	US-11-124-367A-437	Sequence 437, App
585	25	61.0	320	7	US-11-188-298-22463	Sequence 22463, A
586	25	61.0	325	7	US-11-045-004-336	Sequence 336, App
587	25	61.0	328	7	US-11-124-367A-436	Sequence 436, App
588	25	61.0	328	7	US-11-188-298-10318	Sequence 10318, A
589	25	61.0	329	7	US-11-096-568A-11684	Sequence 11684, A
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593	25	61.0	333	7	US-11-188-298-12104	Sequence 12104, A
594	25	61.0	341	7	US-11-087-099-9649	Sequence 9649, Ap
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596	25	61.0	347	7	US-11-087-099-12300	Sequence 12300, A
597	25	61.0	352	7	US-11-087-099-1834	Sequence 1834, Ap
598	25	61.0	352	7	US-11-087-099-2937	Sequence 2937, Ap
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602	25	61.0	357	6	US-10-821-234-1325	Sequence 1325, Ap
603	25	61.0	357	7	US-11-045-004-2501	Sequence 2501, Ap
604	25	61.0	363	7	US-11-188-298-7456	Sequence 7456, Ap
605	25	61.0	364	7	US-11-045-004-2754	Sequence 2754, Ap
606	25	61.0	368	7	US-11-096-568A-22089	Sequence 22089, A
607	25	61.0	368	7	US-11-188-298-14727	Sequence 14727, A
608	25	61.0	369	7	US-11-188-298-17616	Sequence 17616, A
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612	25	61.0	388	7	US-11-096-568A-4730	Sequence 4730, Ap
613	25	61.0	389	7	US-11-096-568A-8051	Sequence 8051, Ap
614	25	61.0	389	7	US-11-188-298-1081	Sequence 1081, Ap
615	25	61.0	391	7	US-11-108-528-12	Sequence 12, Appl
616	25	61.0	391	7	US-11-087-099-11571	Sequence 11571, A
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618	25	61.0	394	6	US-10-506-454-242	Sequence 242, App
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626	25	61.0	405	7	US-11-188-298-10332	Sequence 10332, A
627	25	61.0	405	7	US-11-188-298-11243	Sequence 11243, A
628	25	61.0	406	7	US-11-188-298-21027	Sequence 21027, A
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633	25	61.0	411	7	US-11-087-099-7760	Sequence 7760, Ap
634	25	61.0	411	7	US-11-096-568A-3045	Sequence 3045, Ap
635	25	61.0	411	7	US-11-096-568A-3047	Sequence 3047, Ap
636	25	61.0	411	7	US-11-096-568A-12616	Sequence 12616, A

637	25	61.0	411	7	US-11-188-298-9194	Sequence 9194, Ap
638	25	61.0	412	7	US-11-096-568A-12615	Sequence 12615, A
639	25	61.0	412	7	US-11-188-298-2172	Sequence 2172, Ap
640	25	61.0	413	7	US-11-072-512-2267	Sequence 2267, Ap
641	25	61.0	413	7	US-11-096-568A-11784	Sequence 11784, A
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643	25	61.0	418	7	US-11-096-568A-28266	Sequence 28266, A
644	25	61.0	418	7	US-11-188-298-6616	Sequence 6616, Ap
645	25	61.0	419	6	US-10-821-234-1504	Sequence 1504, Ap
646	25	61.0	422	7	US-11-052-554A-311	Sequence 311, App
647	25	61.0	422	7	US-11-188-298-1399	Sequence 1399, Ap
648	25	61.0	423	6	US-10-506-454-1550	Sequence 1550, Ap
649	25	61.0	424	6	US-10-453-372-68	Sequence 68, Appl
650	25	61.0	424	7	US-11-096-568A-28265	Sequence 28265, A
651	25	61.0	426	7	US-11-188-298-732	Sequence 732, App
652	25	61.0	426	7	US-11-188-298-2607	Sequence 2607, Ap
653	25	61.0	430	7	US-11-096-568A-19483	Sequence 19483, A
654	25	61.0	430	7	US-11-188-298-3939	Sequence 3939, Ap
655	25	61.0	431	6	US-10-467-657-2532	Sequence 2532, Ap
656	25	61.0	433	7	US-11-109-156-9	Sequence 9, Appli
657	25	61.0	435	7	US-11-087-099-1868	Sequence 1868, Ap
658	25	61.0	438	7	US-11-052-554A-310	Sequence 310, App
659	25	61.0	438	7	US-11-096-568A-11315	Sequence 11315, A
660	25	61.0	439	7	US-11-096-568A-4728	Sequence 4728, Ap
661	25	61.0	442	7	US-11-096-568A-11314	Sequence 11314, A
662	25	61.0	442	7	US-11-096-568A-11783	Sequence 11783, A
663	25	61.0	442	7	US-11-188-298-5314	Sequence 5314, Ap
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666	25	61.0	451	7	US-11-096-568A-12614	Sequence 12614, A
667	25	61.0	452	7	US-11-045-004-445	Sequence 445, App
668	25	61.0	453	7	US-11-096-568A-11313	Sequence 11313, A
669	25	61.0	454	7	US-11-188-298-2724	Sequence 2724, Ap
670	25	61.0	469	7	US-11-087-099-4123	Sequence 4123, Ap
671	25	61.0	472	7	US-11-096-568A-7406	Sequence 7406, Ap
672	25	61.0	472	7	US-11-096-568A-19482	Sequence 19482, A
673	25	61.0	474	7	US-11-096-568A-22087	Sequence 22087, A
674	25	61.0	474	7	US-11-188-298-14831	Sequence 14831, A
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676	25	61.0	476	7	US-11-096-568A-10368	Sequence 10368, A
677	25	61.0	477	7	US-11-096-568A-7354	Sequence 7354, Ap
678	25	61.0	481	7	US-11-096-568A-10801	Sequence 10801, A
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680	25	61.0	482	7	US-11-096-568A-3044	Sequence 3044, Ap
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683	25	61.0	489	7	US-11-096-568A-7405	Sequence 7405, Ap
684	25	61.0	491	7	US-11-087-099-6452	Sequence 6452, Ap
685	25	61.0	493	7	US-11-096-568A-8005	Sequence 8005, Ap
686	25	61.0	497	7	US-11-188-298-4298	Sequence 4298, Ap
687	25	61.0	497	7	US-11-188-298-9147	Sequence 9147, Ap
688	25	61.0	497	7	US-11-188-298-11434	Sequence 11434, A
689	25	61.0	498	7	US-11-037-829A-3	Sequence 3, Appli
690	25	61.0	498	7	US-11-122-144-18	Sequence 18, Appl
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692	25	61.0	498	7	US-11-188-298-16162	Sequence 16162, A
693	25	61.0	499	7	US-11-188-298-7015	Sequence 7015, Ap

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695	25	61.0	500	7	US-11-188-298-7304	Sequence 7304, Ap
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697	25	61.0	500	7	US-11-188-298-11524	Sequence 11524, A
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705	25	61.0	503	7	US-11-188-298-16017	Sequence 16017, A
706	25	61.0	503	7	US-11-188-298-19759	Sequence 19759, A
707	25	61.0	504	7	US-11-055-822-136	Sequence 136, App
708	25	61.0	504	7	US-11-261-346-4	Sequence 4, Appli
709	25	61.0	504	7	US-11-188-298-17589	Sequence 17589, A
710	25	61.0	505	7	US-11-087-099-362	Sequence 362, App
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712	25	61.0	510	7	US-11-188-298-12218	Sequence 12218, A
713	25	61.0	510	7	US-11-188-298-20556	Sequence 20556, A
714	25	61.0	511	6	US-10-506-454-796	Sequence 796, App
715	25	61.0	515	7	US-11-188-298-1441	Sequence 1441, Ap
716	25	61.0	521	7	US-11-087-099-4363	Sequence 4363, Ap
717	25	61.0	529	7	US-11-087-099-11190	Sequence 11190, A
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721	25	61.0	531	7	US-11-188-298-9670	Sequence 9670, Ap
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723	25	61.0	539	7	US-11-188-298-9515	Sequence 9515, Ap
724	25	61.0	541	7	US-11-188-298-8461	Sequence 8461, Ap
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726	25	61.0	548	7	US-11-052-554A-324	Sequence 324, App
727	25	61.0	554	6	US-10-506-443A-36	Sequence 36, Appl
728	25	61.0	560	7	US-11-188-298-4932	Sequence 4932, Ap
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730	25	61.0	569	6	US-10-506-443A-35	Sequence 35, Appl
731	25	61.0	575	6	US-10-453-372-78	Sequence 78, Appl
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733	25	61.0	580	7	US-11-072-512-2249	Sequence 2249, Ap
734	25	61.0	586	7	US-11-073-112-18	Sequence 18, Appl
735	25	61.0	587	7	US-11-052-554A-118	Sequence 118, App
736	25	61.0	602	6	US-10-506-454-707	Sequence 707, App
737	25	61.0	611	7	US-11-087-099-8358	Sequence 8358, Ap
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743	25	61.0	645	7	US-11-188-298-2327	Sequence 2327, Ap
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746	25	61.0	648	7	US-11-096-568A-27524	Sequence 27524, A
747	25	61.0	648	7	US-11-188-298-12125	Sequence 12125, A
748	25	61.0	648	7	US-11-188-298-19507	Sequence 19507, A
749	25	61.0	649	6	US-10-063-703-132	Sequence 132, App
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752	25	61.0	649	6	US-10-195-888-384	Sequence 384, App
753	25	61.0	649	6	US-10-195-889-384	Sequence 384, App
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766	25	61.0	686	7	US-11-188-298-7730	Sequence 7730, Ap
767	25	61.0	686	7	US-11-188-298-9628	Sequence 9628, Ap
768	25	61.0	686	7	US-11-188-298-10425	Sequence 10425, A
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797	25	61.0	797	6	US-10-995-561-802	Sequence 802, App
798	25	61.0	797	7	US-11-087-099-9850	Sequence 9850, Ap
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803	25	61.0	807	6	US-10-219-062-188	Sequence 188, App
804	25	61.0	807	6	US-10-219-064-188	Sequence 188, App
805	25	61.0	807	6	US-10-233-134-188	Sequence 188, App
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813	25	61.0	825	7	US-11-124-367A-469	Sequence 469, App
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822	25	61.0	861	7	US-11-188-298-836	Sequence 836, App
823	25	61.0	897	6	US-10-821-234-1523	Sequence 1523, Ap
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826	25	61.0	903	7	US-11-124-367A-450	Sequence 450, App
827	25	61.0	905	6	US-10-330-773-873	Sequence 873, App
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829	25	61.0	936	7	US-11-078-915-16	Sequence 16, Appl
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831	25	61.0	978	7	US-11-078-915-15	Sequence 15, Appl
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834	25	61.0	997	7	US-11-078-915-77	Sequence 77, Appl
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836	25	61.0	998	7	US-11-078-915-8	Sequence 8, Appli
837	25	61.0	998	7	US-11-078-915-9	Sequence 9, Appli
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844	25	61.0	1021	7	US-11-078-915-5	Sequence 5, Appli
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847	25	61.0	1021	7	US-11-078-915-23	Sequence 23, Appl
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852	25	61.0	1142	7	US-11-044-051-73	Sequence 73, Appl
853	25	61.0	1165	7	US-11-197-380-6	Sequence 6, Appli
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857	25	61.0	1323	6	US-10-517-939-312	Sequence 312, App
858	25	61.0	1416	7	US-11-128-059-60	Sequence 60, Appl
859	25	61.0	1433	7	US-11-094-519A-40	Sequence 40, Appl
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868	25	61.0	1731	6	US-10-915-002-192	Sequence 192, App
869	25	61.0	1731	6	US-10-915-002-211	Sequence 211, App
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872	25	61.0	2311	6	US-10-469-469-54	Sequence 54, Appl
873	25	61.0	2313	7	US-11-128-059-80	Sequence 80, Appl
874	25	61.0	2358	7	US-11-128-059-74	Sequence 74, Appl
875	25	61.0	2439	7	US-11-128-059-76	Sequence 76, Appl
876	25	61.0	2458	7	US-11-128-059-94	Sequence 94, Appl
877	25	61.0	2523	7	US-11-052-554A-143	Sequence 143, App
878	25	61.0	2551	6	US-10-453-372-256	Sequence 256, App
879	25	61.0	2551	7	US-11-128-059-96	Sequence 96, Appl
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884	25	61.0	2723	7	US-11-129-741-388	Sequence 388, App
885	25	61.0	2723	7	US-11-129-741-3318	Sequence 3318, Ap
886	25	61.0	2767	7	US-11-100-640-38	Sequence 38, Appl
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889	25	61.0	3157	7	US-11-052-554A-142	Sequence 142, App
890	25	61.0	3507	7	US-11-075-185-7	Sequence 7, Appli
891	25	61.0	3716	7	US-11-052-554A-141	Sequence 141, App
892	25	61.0	4384	6	US-10-821-234-1120	Sequence 1120, Ap
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895	24	58.5	36	6	US-10-989-226-56	Sequence 56, Appl
896	24	58.5	36	7	US-11-066-967-110	Sequence 110, App
897	24	58.5	38	7	US-11-072-175-256	Sequence 256, App
898	24	58.5	61	7	US-11-096-568A-104	Sequence 104, App
899	24	58.5	62	7	US-11-004-399-3212	Sequence 3212, Ap
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901	24	58.5	71	7	US-11-096-568A-11691	Sequence 11691, A
902	24	58.5	83	7	US-11-226-869-62	Sequence 62, Appl
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906	24	58.5	98	6	US-10-816-768-43	Sequence 43, Appl
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908	24	58.5	104	7	US-11-053-076-187	Sequence 187, App
909	24	58.5	112	6	US-10-921-793-76	Sequence 76, Appl
910	24	58.5	112	6	US-10-931-198-76	Sequence 76, Appl
911	24	58.5	112	6	US-10-942-042-76	Sequence 76, Appl
912	24	58.5	113	6	US-10-932-334-66	Sequence 66, Appl
913	24	58.5	113	6	US-10-932-334-68	Sequence 68, Appl
914	24	58.5	115	7	US-11-087-099-1629	Sequence 1629, Ap
915	24	58.5	119	7	US-11-229-769-256	Sequence 256, App
916	24	58.5	121	7	US-11-087-099-3537	Sequence 3537, Ap
917	24	58.5	127	6	US-10-793-626-3322	Sequence 3322, Ap
918	24	58.5	130	7	US-11-098-686-10421	Sequence 10421, A
919	24	58.5	132	6	US-10-330-773-164	Sequence 164, App
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921	24	58.5	138	7	US-11-072-512-2720	Sequence 2720, Ap

922	24	58.5	139	6	US-10-821-234-1674	Sequence 1674, Ap
923	24	58.5	139	7	US-11-072-512-2480	Sequence 2480, Ap
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926	24	58.5	145	6	US-10-703-799B-94	Sequence 94, Appl
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929	24	58.5	150	7	US-11-079-463-6365	Sequence 6365, Ap
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934	24	58.5	159	7	US-11-079-463-7564	Sequence 7564, Ap
935	24	58.5	161	7	US-11-087-099-1739	Sequence 1739, Ap
936	24	58.5	162	6	US-10-454-437-10	Sequence 10, Appl
937	24	58.5	163	7	US-11-096-568A-6776	Sequence 6776, Ap
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942	24	58.5	167	7	US-11-079-463-7048	Sequence 7048, Ap
943	24	58.5	168	7	US-11-079-463-6568	Sequence 6568, Ap
944	24	58.5	169	7	US-11-096-568A-3637	Sequence 3637, Ap
945	24	58.5	170	6	US-10-995-561-564	Sequence 564, App
946	24	58.5	170	7	US-11-120-308-8	Sequence 8, Appli
947	24	58.5	173	7	US-11-087-099-2725	Sequence 2725, Ap
948	24	58.5	173	7	US-11-205-667-3	Sequence 3, Appli
949	24	58.5	174	7	US-11-120-308-30	Sequence 30, Appl
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951	24	58.5	180	7	US-11-096-568A-1163	Sequence 1163, Ap
952	24	58.5	182	7	US-11-096-568A-6775	Sequence 6775, Ap
953	24	58.5	183	7	US-11-087-099-8814	Sequence 8814, Ap
954	24	58.5	185	7	US-11-096-568A-29722	Sequence 29722, A
955	24	58.5	188	7	US-11-096-568A-30245	Sequence 30245, A
956	24	58.5	188	7	US-11-172-740-1625	Sequence 1625, Ap
957	24	58.5	189	7	US-11-098-686-10887	Sequence 10887, A
958	24	58.5	190	7	US-11-120-308-26	Sequence 26, Appl
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962	24	58.5	207	7	US-11-045-004-375	Sequence 375, App
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964	24	58.5	209	7	US-11-096-568A-6774	Sequence 6774, Ap
965	24	58.5	209	7	US-11-096-568A-23262	Sequence 23262, A
966	24	58.5	209	7	US-11-079-463-5358	Sequence 5358, Ap
967	24	58.5	211	7	US-11-096-568A-13702	Sequence 13702, A
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969	24	58.5	213	7	US-11-096-568A-5891	Sequence 5891, Ap
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971	24	58.5	216	6	US-10-467-657-1284	Sequence 1284, Ap
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973	24	58.5	216	6	US-10-467-657-7492	Sequence 7492, Ap
974	24	58.5	216	6	US-10-467-657-8232	Sequence 8232, Ap
975	24	58.5	216	6	US-10-467-657-8310	Sequence 8310, Ap
976	24	58.5	217	7	US-11-072-512-3043	Sequence 3043, Ap
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982	24	58.5	233	7	US-11-096-568A-11371	Sequence 11371, A
983	24	58.5	235	7	US-11-096-568A-5890	Sequence 5890, Ap
984	24	58.5	235	7	US-11-096-568A-21210	Sequence 21210, A
985	24	58.5	237	6	US-10-506-454-1600	Sequence 1600, Ap
986	24	58.5	238	7	US-11-195-585-16	Sequence 16, Appl
987	24	58.5	239	7	US-11-096-568A-5889	Sequence 5889, Ap
988	24	58.5	240	7	US-11-223-680-4	Sequence 4, Appli
989	24	58.5	240	7	US-11-072-512-3712	Sequence 3712, Ap
990	24	58.5	240	7	US-11-096-568A-21174	Sequence 21174, A
991	24	58.5	241	7	US-11-096-568A-29721	Sequence 29721, A
992	24	58.5	242	7	US-11-096-568A-26110	Sequence 26110, A
993	24	58.5	243	7	US-11-096-568A-1162	Sequence 1162, Ap
994	24	58.5	245	7	US-11-096-568A-1161	Sequence 1161, Ap
995	24	58.5	249	7	US-11-054-515-493	Sequence 493, App
996	24	58.5	249	7	US-11-266-444-493	Sequence 493, App
997	24	58.5	250	7	US-11-054-515-1484	Sequence 1484, Ap
998	24	58.5	250	7	US-11-098-686-11306	Sequence 11306, A
999	24	58.5	250	7	US-11-266-444-1484	Sequence 1484, Ap
1000	24	58.5	251	7	US-11-096-568A-21502	Sequence 21502, A

ALIGNMENTS

RESULT 1

US-11-079-463-9097

; Sequence 9097, Application US/11079463

; Publication No. US20060073161A1

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
BACTEROIDES FRAGILIS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: PATH00-03DIV2

; CURRENT APPLICATION NUMBER: US/11/079,463

; CURRENT FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/128,705

; PRIOR FILING DATE: 1999-04-09

; PRIOR APPLICATION NUMBER: US 09/540,209

; PRIOR FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 10444

; SEQ ID NO 9097

; LENGTH: 329

; TYPE: PRT

; ORGANISM: B.fragilis

US-11-079-463-9097

Query Match 85.4%; Score 35; DB 7; Length 329;

Best Local Similarity 75.0%; Pred. No. 19;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

||||:|:

Db 103 NAPVTIPE 110

RESULT 2

US-11-110-082-38

; Sequence 38, Application US/11110082
 ; Publication No. US20050266558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Demmer, Jeroen
 ; APPLICANT: Hall, Claire
 ; APPLICANT: Norriss, Michael Geoffrey
 ; APPLICANT: Saulsbury, Keith Martin
 ; TITLE OF INVENTION: Compositions Isolated from Forage
 ; TITLE OF INVENTION: Grasses and methods for their use.
 ; FILE REFERENCE: 11000.1074Uc1
 ; CURRENT APPLICATION NUMBER: US/11/110,082
 ; CURRENT FILING DATE: 2005-04-19
 ; PRIOR APPLICATION NUMBER: 60/563,723
 ; PRIOR FILING DATE: 2004-04-20
 ; PRIOR APPLICATION NUMBER: 10/655,799
 ; PRIOR FILING DATE: 2003-09-05
 ; PRIOR APPLICATION NUMBER: 60/408,782
 ; PRIOR FILING DATE: 2002-09-05
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 808
 ; TYPE: PRT
 ; ORGANISM: Festuca arundinacea

US-11-110-082-38

Query Match 85.4%; Score 35; DB 7; Length 808;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |:|:|:|
 Db 271 NSPVAIPQ 278

RESULT 3

US-11-188-298-5829

; Sequence 5829, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 5829
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Glycine max

US-11-188-298-5829

Query Match 82.9%; Score 34; DB 7; Length 503;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||||:
Db 133 NAPVSLP 139

RESULT 4

US-11-188-298-9524
; Sequence 9524, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 9524
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(503)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-9524

Query Match 82.9%; Score 34; DB 7; Length 503;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||||:
Db 133 NAPVSLP 139

RESULT 5

US-11-188-298-13806
; Sequence 13806, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13806
; LENGTH: 503

; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-188-298-13806

Query Match 82.9%; Score 34; DB 7; Length 503;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|
Db 133 NAPVSLP 139

RESULT 6

US-11-188-298-17178
; Sequence 17178, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17178
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(512)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-17178

Query Match 82.9%; Score 34; DB 7; Length 512;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|
Db 141 NAPVSLP 147

RESULT 7

US-11-188-298-5631
; Sequence 5631, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31

; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 5631
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-188-298-5631

Query Match 82.9%; Score 34; DB 7; Length 641;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|
Db 133 NAPVSLP 139

RESULT 8

US-10-821-234-1624
; Sequence 1624, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1624
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1624

Query Match 80.5%; Score 33; DB 6; Length 574;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:
Db 500 NSPVSLPE 507

RESULT 9

US-11-143-980-44
; Sequence 44, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.

```
; APPLICANT:  Graziani, Edmund
; APPLICANT:  Summers, Mia
; APPLICANT:  Kulowski, Kerry
; APPLICANT:  Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; TITLE OF INVENTION: Polyketide
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-11-143-980-44
```

```
Query Match          78.0%; Score 32; DB 7; Length 476;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches      5; Conservative      2; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||| :|:
Db      383 NAPVGLPE 390
```

RESULT 10

```
US-11-096-568A-12983
; Sequence 12983, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12983
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(513)
; OTHER INFORMATION: Ceres Seq. ID no. 14314103
US-11-096-568A-12983
```

```
Query Match          78.0%; Score 32; DB 7; Length 513;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches      6; Conservative      1; Mismatches      1; Indels      0; Gaps      0;
```

Qy 1 NAPVSIPQ 8
: || |||
Db 38 DAPASIPQ 45

RESULT 11

US-11-096-568A-12982
; Sequence 12982, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12982
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(548)
; OTHER INFORMATION: Ceres Seq. ID no. 14314102
US-11-096-568A-12982

Query Match 78.0%; Score 32; DB 7; Length 548;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
: || |||
Db 73 DAPASIPQ 80

RESULT 12

US-11-096-568A-12981
; Sequence 12981, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12981
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(613)

; OTHER INFORMATION: Ceres Seq. ID no. 14314101
US-11-096-568A-12981

Query Match 78.0%; Score 32; DB 7; Length 613;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
: || ||||
Db 138 DAPASIPQ 145

RESULT 13

US-10-467-657-6986

; Sequence 6986, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6986
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6986

Query Match 75.6%; Score 31; DB 6; Length 358;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
||| |:|
Db 142 NAPASVP 148

RESULT 14

US-11-188-298-21875

; Sequence 21875, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31

; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 21875
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Sorghum bicolor
US-11-188-298-21875

Query Match 75.6%; Score 31; DB 7; Length 424;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|:|:|:|
Db 40 NSPVSLP 46

RESULT 15

US-10-506-454-1067
; Sequence 1067, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the
Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal
Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1067
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1067

Query Match 75.6%; Score 31; DB 6; Length 481;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 370 NAPVFPVE 377

RESULT 16

US-11-188-298-5842

; Sequence 5842, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 5842
 ; LENGTH: 487
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-11-188-298-5842

Query Match 75.6%; Score 31; DB 7; Length 487;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 |:|:|:|
 Db 117 NSPVSLP 123

RESULT 17

US-11-188-298-15955

; Sequence 15955, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 15955
 ; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-11-188-298-15955

Query Match 75.6%; Score 31; DB 7; Length 505;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 |:|:|:|
 Db 135 NSPVSLP 141

RESULT 18

US-11-188-298-3808
 ; Sequence 3808, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 3808
 ; LENGTH: 506
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(506)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-11-188-298-3808

Query Match 75.6%; Score 31; DB 7; Length 506;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIP 7
 |:|:|:|
 Db 136 NSPVSLP 142

RESULT 19
 US-11-188-298-14719
 ; Sequence 14719, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 14719
 ; LENGTH: 511
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(511)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-11-188-298-14719

Query Match 75.6%; Score 31; DB 7; Length 511;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|:|:|:|
Db 138 NSPVSLP 144

RESULT 20

US-10-793-626-532
; Sequence 532, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 532
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-532

Query Match 75.6%; Score 31; DB 6; Length 521;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 96 NKPVSIP 102

RESULT 21

US-11-068-783-39
; Sequence 39, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: PRT

; ORGANISM: Apis mellifera
US-11-068-783-39

Query Match 73.2%; Score 30; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | |
Db 3 NRPVYIPQ 10

RESULT 22

US-11-068-783-40

; Sequence 40, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apis mellifera
US-11-068-783-40

Query Match 73.2%; Score 30; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | |
Db 3 NRPVYIPQ 10

RESULT 23

US-11-153-071-12

; Sequence 12, Application US/11153071
; Publication No. US20060064773A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Mei
; APPLICANT: Simmons, Carl
; APPLICANT: Hershey, Howard
; TITLE OF INVENTION: Cell Cycle Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Methods of Use Thereof
; FILE REFERENCE: 1874
; CURRENT APPLICATION NUMBER: US/11/153,071
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/583,340

; PRIOR FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Zea mays
US-11-153-071-12

Query Match 73.2%; Score 30; DB 7; Length 239;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | : | |
Db 33 NQPVHVPQ 40

RESULT 24

US-11-096-568A-3188
; Sequence 3188, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3188
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(250)
; OTHER INFORMATION: Ceres Seq. ID no. 14305859
US-11-096-568A-3188

Query Match 73.2%; Score 30; DB 7; Length 250;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
: | | : | | :
Db 51 DAPISLPE 58

RESULT 25

US-11-096-568A-3189
; Sequence 3189, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.

```

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3189
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(250)
; OTHER INFORMATION: Ceres Seq. ID no. 16625457
US-11-096-568A-3189

```

```

Query Match          73.2%; Score 30; DB 7; Length 250;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches      4; Conservative      4; Mismatches      0; Indels      0; Gaps      0;

```

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Qy      1 NAPVSIPQ 8
        :||:|:|:
Db      51 DAPISLPE 58

```

RESULT 26

```

US-10-714-887-304
; Sequence 304, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MBI0058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22

```

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; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 304
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G1075 polypeptide Functionally related and homologous to
G1073
US-10-714-887-304

```

```

Query Match          73.2%; Score 30; DB 6; Length 285;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches      5; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        | | : | : |
Db      260 NLPMSMPQ 267

```

RESULT 27

```

US-11-052-554A-131
; Sequence 131, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-
LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Mycoplasma pneumoniae
US-11-052-554A-131

```

```

Query Match          73.2%; Score 30; DB 7; Length 322;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;

```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
:||||:
Db 29 SAPVSV 35

RESULT 28

US-11-188-298-10980

; Sequence 10980, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10980
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Hordeum vulgare subsp. vulgare
US-11-188-298-10980

Query Match 73.2%; Score 30; DB 7; Length 339;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
|||||:
Db 10 APVSLPE 16

RESULT 29

US-10-821-234-1569

; Sequence 1569, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1569
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1569

Query Match 73.2%; Score 30; DB 6; Length 367;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 340 NFPVSIP 346

RESULT 30

US-11-188-298-4486
; Sequence 4486, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 4486
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-11-188-298-4486

Query Match 73.2%; Score 30; DB 7; Length 482;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 152 NFPVSIP 158

RESULT 31

US-11-087-099-9607
; Sequence 9607, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9607
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Thermoanaerobacter brockii
US-11-087-099-9607

Query Match 73.2%; Score 30; DB 7; Length 730;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|:||||
Db 546 PISIPQ 551

RESULT 32

US-11-188-298-8921

; Sequence 8921, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8921
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Thermoanaerobacter brockii
US-11-188-298-8921

Query Match 73.2%; Score 30; DB 7; Length 730;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|:||||
Db 546 PISIPQ 551

RESULT 33

US-11-087-099-3348

; Sequence 3348, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3348
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Thermoanaerobacter ethanolicus
US-11-087-099-3348

Query Match 73.2%; Score 30; DB 7; Length 784;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8

Db |:||||
600 PISIPQ 605

RESULT 34

US-11-188-298-20082
; Sequence 20082, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20082
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Thermoanaerobacter ethanolicus
US-11-188-298-20082

Query Match 73.2%; Score 30; DB 7; Length 784;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
 |:||||
Db 600 PISIPQ 605

RESULT 35

US-10-649-591-16
; Sequence 16, Application US/10649591
; Publication No. US20060035237A1
; GENERAL INFORMATION:
; APPLICANT: Markowitz, Sanford D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P03-003
; CURRENT APPLICATION NUMBER: US/10/649,591
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 10/229,345
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 10/274,177
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-649-591-16

Query Match 73.2%; Score 30; DB 6; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 36

US-10-501-035-379

; Sequence 379, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR
PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN
TYROSINE KINASES
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 379
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-379

Query Match 73.2%; Score 30; DB 6; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 37

US-11-090-739-122

; Sequence 122, Application US/11090739
; Publication No. US20050260639A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke
; APPLICANT: KATAGIRI, Toyomasa
; APPLICANT: NAKAGAWA, Hidewaki
; TITLE OF INVENTION: METHOD FOR DIAGNOSING PANCREATIC CANCER
; FILE REFERENCE: 082368-003600US
; CURRENT APPLICATION NUMBER: US/11/090,739
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP2003/011817
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/555,809
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/450,889

; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,872
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-739-122

Query Match 73.2%; Score 30; DB 7; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 38

US-11-186-284-18
; Sequence 18, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-18

Query Match 73.2%; Score 30; DB 7; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 39

US-11-200-822-1

; Sequence 1, Application US/11200822
; Publication No. US20060040302A1
; GENERAL INFORMATION:
; APPLICANT: Bostein, et al.
; TITLE OF INVENTION: Methods of Classifying, Diagnosing, Stratifying and
; TITLE OF INVENTION: Treating Cancer Patients and Their Tumors
; FILE REFERENCE: 2002850-0049
; CURRENT APPLICATION NUMBER: US/11/200,822
; CURRENT FILING DATE: 2005-08-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Sequence of
; OTHER INFORMATION: Cadherin 3

US-11-200-822-1

Query Match 73.2%; Score 30; DB 7; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 40

US-11-264-046-1

; Sequence 1, Application US/11264046
; Publication No. US20060039915A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Klinger, Julie
; APPLICANT: Jefferson, Ann
; APPLICANT: Escobedo, Jaime
; APPLICANT: Randazzo, Fillipo
; APPLICANT: Winter, Jill
; APPLICANT: Goodson, Robert
; APPLICANT: Qi, Weimin
; TITLE OF INVENTION: P-Cadherin as a Target for Anti-Cancer
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 35784/258994
; CURRENT APPLICATION NUMBER: US/11/264,046
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: US/10/158,123

; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,225
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-046-1

Query Match 73.2%; Score 30; DB 7; Length 829;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|:
Db 112 APISVPE 118

RESULT 41

US-11-188-298-12858
; Sequence 12858, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12858
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-188-298-12858

Query Match 73.2%; Score 30; DB 7; Length 868;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| |||||
Db 595 NNPVSIP 601

RESULT 42

US-11-188-298-20296
; Sequence 20296, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298

; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20296
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-188-298-20296

Query Match 73.2%; Score 30; DB 7; Length 869;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| |||:
Db 28 NRPVSV 34

RESULT 43

US-11-096-568A-31020
; Sequence 31020, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polypeptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31020
; LENGTH: 927
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(927)
; OTHER INFORMATION: Ceres Seq. ID no. 4983911
US-11-096-568A-31020

Query Match 73.2%; Score 30; DB 7; Length 927;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| |:::
Db 446 NVPISLPK 453

RESULT 44

US-11-207-626A-44
; Sequence 44, Application US/11207626A
; Publication No. US20060014276A1
; GENERAL INFORMATION:
; APPLICANT: Havenga, Menzo

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; APPLICANT: Vogels, Ronald
; APPLICANT: Bout, Abraham
; TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
; FILE REFERENCE: 2578-4123.2US
; CURRENT APPLICATION NUMBER: US/11/207,626A
; CURRENT FILING DATE: 2005-08-18
; PRIOR APPLICATION NUMBER: EP 98202297.2
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
;   LENGTH: 946
;   TYPE: PRT
;   ORGANISM: Human Adenovirus 35 Hexon Protein
US-11-207-626A-44
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Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;
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Qy          1 NAPVSIP 7
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Db          663 NIPISIP 669
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RESULT 45

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US-11-207-626A-45
; Sequence 45, Application US/11207626A
; Publication No. US20060014276A1
; GENERAL INFORMATION:
; APPLICANT: Havenga, Menzo
; APPLICANT: Vogels, Ronald
; APPLICANT: Bout, Abraham
; TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
; FILE REFERENCE: 2578-4123.2US
; CURRENT APPLICATION NUMBER: US/11/207,626A
; CURRENT FILING DATE: 2005-08-18
; PRIOR APPLICATION NUMBER: EP 98202297.2
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 952
;   TYPE: PRT
;   ORGANISM: Human Adenovirus 36 Hexon Protein
US-11-207-626A-45
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Query Match          73.2%; Score 30; DB 7; Length 952;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;
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Qy          1 NAPVSIP 7
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Db          667 NIPISIP 673
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RESULT 46

US-11-207-626A-43
 ; Sequence 43, Application US/11207626A
 ; Publication No. US20060014276A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Havenga, Menzo
 ; APPLICANT: Vogels, Ronald
 ; APPLICANT: Bout, Abraham
 ; TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
 ; FILE REFERENCE: 2578-4123.2US
 ; CURRENT APPLICATION NUMBER: US/11/207,626A
 ; CURRENT FILING DATE: 2005-08-18
 ; PRIOR APPLICATION NUMBER: EP 98202297.2
 ; PRIOR FILING DATE: 1998-07-08
 ; NUMBER OF SEQ ID NOS: 87
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 43
 ; LENGTH: 958
 ; TYPE: PRT
 ; ORGANISM: Human Adenovirus 34 Hexon Protein
 US-11-207-626A-43

Query Match 73.2%; Score 30; DB 7; Length 958;
 Best Local Similarity 71.4%; Pred. No. 5.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
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 Db 673 NIPISIP 679

RESULT 47
 US-11-188-298-4720
 ; Sequence 4720, Application US/11188298
 ; Publication No. US20060075522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53452)B
 ; CURRENT APPLICATION NUMBER: US/11/188,298
 ; CURRENT FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: 60/592,978
 ; PRIOR FILING DATE: 2004-07-31
 ; NUMBER OF SEQ ID NOS: 22569
 ; SEQ ID NO 4720
 ; LENGTH: 963
 ; TYPE: PRT
 ; ORGANISM: Eremothecium gossypii
 US-11-188-298-4720

Query Match 73.2%; Score 30; DB 7; Length 963;
 Best Local Similarity 85.7%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 | | | | |
 Db 700 NNPVSIP 706

RESULT 48

US-11-096-568A-31019

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; Sequence 31019, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polyptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31019
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1005)
; OTHER INFORMATION: Ceres Seq. ID no. 4983910
US-11-096-568A-31019
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Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches      4; Conservative      3; Mismatches      1; Indels      0; Gaps      0;
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Qy      1 NAPVSIPQ 8
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Db      524 NVPISLPK 531
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RESULT 49

US-11-096-568A-31018

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; Sequence 31018, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
Polyptides Encoded
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31018
; LENGTH: 1007
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1007)
; OTHER INFORMATION: Ceres Seq. ID no. 4983909
US-11-096-568A-31018
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Query Match          73.2%; Score 30; DB 7; Length 1007;
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Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | : | :
Db 526 NVPISLPK 533

RESULT 50

US-11-052-554A-123
; Sequence 123, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-
LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-11-052-554A-123

Query Match 73.2%; Score 30; DB 7; Length 1218;
Best Local Similarity 71.4%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
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Db 323 SAPVSV 329

Search completed: April 26, 2006, 00:27:04
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: April 26, 2006, 00:22:38 ; Search time 47 Seconds
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Title: US-10-748-765-2
Perfect score: 41
Sequence: 1 NAPVSIPQ 8

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Searched: 572060 seqs, 82675679 residues

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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	41	100.0	10	2	US-09-187-330-33	Sequence 33, Appl
4	41	100.0	10	2	US-09-267-511-23	Sequence 23, Appl
5	41	100.0	13	2	US-09-187-330-34	Sequence 34, Appl
6	41	100.0	13	2	US-09-267-511-24	Sequence 24, Appl
7	41	100.0	15	2	US-09-187-330-35	Sequence 35, Appl
8	41	100.0	15	2	US-09-267-511-25	Sequence 25, Appl
9	41	100.0	17	2	US-09-267-511-19	Sequence 19, Appl
10	41	100.0	17	2	US-09-267-511-26	Sequence 26, Appl
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16	41	100.0	726	2	US-09-187-330-57	Sequence 57, Appl
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18	41	100.0	787	2	US-09-187-330-31	Sequence 31, Appl
19	41	100.0	800	2	US-09-187-330-41	Sequence 41, Appl
20	41	100.0	806	2	US-09-187-330-3	Sequence 3, Appli
21	41	100.0	828	2	US-09-187-330-55	Sequence 55, Appl
22	41	100.0	874	2	US-09-187-330-59	Sequence 59, Appl
23	41	100.0	1000	2	US-09-187-330-1	Sequence 1, Appli
24	41	100.0	1102	2	US-09-364-609-8	Sequence 8, Appli
25	36	87.8	9	2	US-09-187-330-28	Sequence 28, Appl
26	36	87.8	360	2	US-09-252-991A-31993	Sequence 31993, A
27	36	87.8	510	2	US-09-634-238-237	Sequence 237, App
28	36	87.8	510	2	US-10-169-048-18	Sequence 18, Appl
29	36	87.8	519	2	US-09-134-000C-6226	Sequence 6226, Ap
30	34	82.9	469	2	US-09-328-352-4822	Sequence 4822, Ap
31	34	82.9	849	2	US-09-949-016-9522	Sequence 9522, Ap
32	33	80.5	205	2	US-09-489-039A-7548	Sequence 7548, Ap
33	33	80.5	295	2	US-09-808-387-20	Sequence 20, Appl
34	33	80.5	344	2	US-09-808-387-12	Sequence 12, Appl
35	33	80.5	344	2	US-09-808-387-18	Sequence 18, Appl
36	33	80.5	386	2	US-09-808-387-6	Sequence 6, Appli
37	33	80.5	481	2	US-09-489-039A-9148	Sequence 9148, Ap
38	33	80.5	557	2	US-09-808-387-4	Sequence 4, Appli
39	33	80.5	557	2	US-09-808-387-10	Sequence 10, Appl
40	33	80.5	574	2	US-09-808-387-2	Sequence 2, Appli
41	33	80.5	574	2	US-09-808-387-8	Sequence 8, Appli
42	33	80.5	574	2	US-09-808-387-16	Sequence 16, Appl
43	31	75.6	114	2	US-09-270-767-33696	Sequence 33696, A
44	31	75.6	114	2	US-09-270-767-48913	Sequence 48913, A
45	31	75.6	292	2	US-09-328-352-8057	Sequence 8057, Ap
46	31	75.6	306	2	US-09-248-796A-24473	Sequence 24473, A
47	31	75.6	317	2	US-09-543-681A-4789	Sequence 4789, Ap
48	31	75.6	376	2	US-09-489-039A-7535	Sequence 7535, Ap
49	31	75.6	392	2	US-09-600-099-6	Sequence 6, Appli
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51	31	75.6	459	6	5194375-6	Patent No. 5194375
52	31	75.6	521	2	US-09-710-279-532	Sequence 532, App
53	31	75.6	525	2	US-09-134-001C-3514	Sequence 3514, Ap
54	31	75.6	881	1	US-08-333-901-1	Sequence 1, Appli
55	31	75.6	881	1	US-08-456-582-1	Sequence 1, Appli
56	31	75.6	881	1	US-08-898-789-1	Sequence 1, Appli
57	31	75.6	881	2	US-09-039-555B-16	Sequence 16, Appl
58	31	75.6	881	2	US-09-324-258-7	Sequence 7, Appli
59	31	75.6	951	2	US-08-816-346-58	Sequence 58, Appl
60	31	75.6	951	2	US-09-335-411-58	Sequence 58, Appl
61	31	75.6	952	1	US-08-788-674-5	Sequence 5, Appli
62	31	75.6	952	2	US-08-816-346-4	Sequence 4, Appli
63	31	75.6	952	2	US-09-335-411-4	Sequence 4, Appli
64	31	75.6	967	2	US-08-816-346-56	Sequence 56, Appl
65	31	75.6	967	2	US-09-335-411-56	Sequence 56, Appl
66	31	75.6	968	2	US-08-816-346-2	Sequence 2, Appli
67	31	75.6	968	2	US-09-335-411-2	Sequence 2, Appli
68	31	75.6	1179	2	US-09-107-532A-6126	Sequence 6126, Ap

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73	30	73.2	18	2	US-09-030-619-96	Sequence 96, Appl
74	30	73.2	18	2	US-09-030-619-158	Sequence 158, App
75	30	73.2	18	2	US-09-030-619-159	Sequence 159, App
76	30	73.2	18	2	US-09-485-147A-42	Sequence 42, Appl
77	30	73.2	18	2	US-10-225-087-1	Sequence 1, Appli
78	30	73.2	18	2	US-09-444-281-39	Sequence 39, Appl
79	30	73.2	18	2	US-09-444-281-40	Sequence 40, Appl
80	30	73.2	18	4	PCT-US95-02626-23	Sequence 23, Appl
81	30	73.2	18	4	PCT-US95-02626-24	Sequence 24, Appl
82	30	73.2	78	2	US-09-248-796A-26514	Sequence 26514, A
83	30	73.2	108	2	US-08-893-534A-4	Sequence 4, Appli
84	30	73.2	108	2	US-08-996-679-4	Sequence 4, Appli
85	30	73.2	108	2	US-08-939-853A-6	Sequence 6, Appli
86	30	73.2	108	2	US-09-115-395-4	Sequence 4, Appli
87	30	73.2	108	2	US-09-113-977C-37	Sequence 37, Appl
88	30	73.2	108	2	US-09-507-102-4	Sequence 4, Appli
89	30	73.2	108	2	US-09-250-059-4	Sequence 4, Appli
90	30	73.2	108	2	US-09-248-074-4	Sequence 4, Appli
91	30	73.2	108	2	US-09-357-717-4	Sequence 4, Appli
92	30	73.2	108	2	US-09-458-870-4	Sequence 4, Appli
93	30	73.2	108	2	US-09-351-048A-37	Sequence 37, Appl
94	30	73.2	108	2	US-09-248-015-4	Sequence 4, Appli
95	30	73.2	108	2	US-09-544-782-4	Sequence 4, Appli
96	30	73.2	108	2	US-10-058-821-4	Sequence 4, Appli
97	30	73.2	108	2	US-10-193-653-37	Sequence 37, Appl
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102	30	73.2	365	2	US-09-328-352-6107	Sequence 6107, Ap
103	30	73.2	367	1	US-08-530-290-24	Sequence 24, Appl
104	30	73.2	367	1	US-08-990-379-6	Sequence 6, Appli
105	30	73.2	367	2	US-09-919-497-60	Sequence 60, Appl
106	30	73.2	449	2	US-09-949-016-10840	Sequence 10840, A
107	30	73.2	488	1	US-08-115-365-2	Sequence 2, Appli
108	30	73.2	488	1	US-08-586-897-2	Sequence 2, Appli
109	30	73.2	488	2	US-09-826-509-561	Sequence 561, App
110	30	73.2	489	2	US-09-393-171-7	Sequence 7, Appli
111	30	73.2	513	1	US-08-390-162-6	Sequence 6, Appli
112	30	73.2	513	1	US-08-685-945B-6	Sequence 6, Appli
113	30	73.2	666	2	US-09-134-000C-6159	Sequence 6159, Ap
114	30	73.2	815	2	US-09-339-159B-26	Sequence 26, Appl
115	30	73.2	821	1	US-07-935-311A-4	Sequence 4, Appli
116	30	73.2	821	1	US-08-368-079-4	Sequence 4, Appli
117	30	73.2	821	2	US-09-886-319A-33	Sequence 33, Appl
118	30	73.2	821	4	PCT-US93-07996-4	Sequence 4, Appli
119	30	73.2	904	2	US-09-252-991A-19257	Sequence 19257, A
120	29	70.7	18	1	US-08-205-938A-25	Sequence 25, Appl
121	29	70.7	18	2	US-09-030-619-160	Sequence 160, App
122	29	70.7	18	2	US-09-444-281-41	Sequence 41, Appl
123	29	70.7	18	4	PCT-US95-02626-25	Sequence 25, Appl
124	29	70.7	59	2	US-09-270-767-45960	Sequence 45960, A
125	29	70.7	137	2	US-09-248-796A-22240	Sequence 22240, A

126	29	70.7	209	2	US-09-248-796A-24512	Sequence 24512, A
127	29	70.7	221	2	US-09-543-681A-4319	Sequence 4319, Ap
128	29	70.7	227	2	US-09-328-352-6446	Sequence 6446, Ap
129	29	70.7	268	2	US-09-252-991A-30798	Sequence 30798, A
130	29	70.7	310	2	US-09-248-796A-20719	Sequence 20719, A
131	29	70.7	383	2	US-09-902-540-10115	Sequence 10115, A
132	29	70.7	418	2	US-09-328-352-7644	Sequence 7644, Ap
133	29	70.7	425	2	US-09-252-991A-25840	Sequence 25840, A
134	29	70.7	449	2	US-09-270-767-57465	Sequence 57465, A
135	29	70.7	491	2	US-09-489-039A-12234	Sequence 12234, A
136	29	70.7	560	1	US-09-132-619-10	Sequence 10, Appl
137	29	70.7	560	2	US-09-282-803B-10	Sequence 10, Appl
138	29	70.7	560	2	US-09-510-654-10	Sequence 10, Appl
139	29	70.7	601	2	US-09-270-767-42194	Sequence 42194, A
140	29	70.7	660	2	US-09-902-540-14368	Sequence 14368, A
141	29	70.7	682	2	US-09-270-767-45389	Sequence 45389, A
142	29	70.7	814	2	US-09-328-352-4373	Sequence 4373, Ap
143	29	70.7	824	2	US-09-399-081A-8	Sequence 8, Appli
144	29	70.7	873	2	US-09-248-796A-20365	Sequence 20365, A
145	29	70.7	905	1	US-08-574-959A-9	Sequence 9, Appli
146	29	70.7	905	2	US-09-357-014-9	Sequence 9, Appli
147	29	70.7	1135	1	US-08-574-959A-7	Sequence 7, Appli
148	29	70.7	1135	2	US-09-357-014-7	Sequence 7, Appli
149	29	70.7	2289	2	US-09-051-019-2	Sequence 2, Appli
150	29	70.7	4019	2	US-09-854-133-425	Sequence 425, App
151	28	68.3	20	2	US-08-899-279-18	Sequence 18, Appl
152	28	68.3	20	2	US-08-899-279-18	Sequence 18, Appl
153	28	68.3	20	2	US-10-047-403-18	Sequence 18, Appl
154	28	68.3	44	2	US-09-865-621A-22	Sequence 22, Appl
155	28	68.3	53	2	US-09-105-470B-13	Sequence 13, Appl
156	28	68.3	108	2	US-09-270-767-60069	Sequence 60069, A
157	28	68.3	111	2	US-09-270-767-39638	Sequence 39638, A
158	28	68.3	111	2	US-09-270-767-54855	Sequence 54855, A
159	28	68.3	139	2	US-09-252-991A-18208	Sequence 18208, A
160	28	68.3	143	2	US-09-332-063-4	Sequence 4, Appli
161	28	68.3	152	2	US-09-270-767-36321	Sequence 36321, A
162	28	68.3	152	2	US-09-270-767-51538	Sequence 51538, A
163	28	68.3	167	1	US-08-993-228-8	Sequence 8, Appli
164	28	68.3	169	2	US-09-252-991A-21582	Sequence 21582, A
165	28	68.3	191	2	US-09-248-796A-14247	Sequence 14247, A
166	28	68.3	194	1	US-08-272-255-20	Sequence 20, Appl
167	28	68.3	194	4	PCT-US95-08565-20	Sequence 20, Appl
168	28	68.3	216	2	US-09-252-991A-23468	Sequence 23468, A
169	28	68.3	243	2	US-09-328-352-7058	Sequence 7058, Ap
170	28	68.3	272	2	US-09-248-796A-21180	Sequence 21180, A
171	28	68.3	301	2	US-09-248-796A-18853	Sequence 18853, A
172	28	68.3	309	2	US-09-902-540-11246	Sequence 11246, A
173	28	68.3	333	2	US-09-902-540-10539	Sequence 10539, A
174	28	68.3	353	2	US-10-104-047-2052	Sequence 2052, Ap
175	28	68.3	363	2	US-09-248-796A-18535	Sequence 18535, A
176	28	68.3	374	1	US-07-914-281-11	Sequence 11, Appl
177	28	68.3	374	1	US-08-393-246-11	Sequence 11, Appl
178	28	68.3	374	1	US-08-525-058A-11	Sequence 11, Appl
179	28	68.3	374	1	US-08-696-731-11	Sequence 11, Appl
180	28	68.3	374	2	US-09-042-531-11	Sequence 11, Appl
181	28	68.3	377	2	US-09-134-000C-6222	Sequence 6222, Ap
182	28	68.3	389	2	US-09-712-363-196	Sequence 196, App

183	28	68.3	411	2	US-09-902-540-15186	Sequence 15186, A
184	28	68.3	429	2	US-09-328-352-8033	Sequence 8033, Ap
185	28	68.3	471	2	US-09-513-007-2	Sequence 2, Appli
186	28	68.3	471	2	US-09-538-092-1295	Sequence 1295, Ap
187	28	68.3	471	2	US-09-970-532-2	Sequence 2, Appli
188	28	68.3	496	2	US-09-540-236-2840	Sequence 2840, Ap
189	28	68.3	502	2	US-09-270-767-44620	Sequence 44620, A
190	28	68.3	531	2	US-09-248-796A-17436	Sequence 17436, A
191	28	68.3	549	2	US-10-104-047-3526	Sequence 3526, Ap
192	28	68.3	624	2	US-09-970-367-6	Sequence 6, Appli
193	28	68.3	663	2	US-08-933-711B-16	Sequence 16, Appl
194	28	68.3	675	2	US-09-332-063-2	Sequence 2, Appli
195	28	68.3	675	2	US-09-332-063-3	Sequence 3, Appli
196	28	68.3	700	2	US-08-933-711B-5	Sequence 5, Appli
197	28	68.3	700	2	US-08-933-711B-6	Sequence 6, Appli
198	28	68.3	757	2	US-09-494-297A-2	Sequence 2, Appli
199	28	68.3	772	2	US-09-134-078-28	Sequence 28, Appl
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203	28	68.3	1055	2	US-09-902-540-15453	Sequence 15453, A
204	28	68.3	1153	2	US-09-362-842-8	Sequence 8, Appli
205	28	68.3	1224	2	US-09-902-540-16312	Sequence 16312, A
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207	27	65.9	16	2	US-09-946-678-4	Sequence 4, Appli
208	27	65.9	37	2	US-08-905-223-22	Sequence 22, Appl
209	27	65.9	37	2	US-09-247-155-22	Sequence 22, Appl
210	27	65.9	37	2	US-09-663-600A-22	Sequence 22, Appl
211	27	65.9	37	2	US-09-903-190-22	Sequence 22, Appl
212	27	65.9	50	2	US-09-261-855-25	Sequence 25, Appl
213	27	65.9	50	2	US-09-873-637-25	Sequence 25, Appl
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216	27	65.9	72	2	US-09-489-039A-9351	Sequence 9351, Ap
217	27	65.9	78	2	US-09-513-999C-5875	Sequence 5875, Ap
218	27	65.9	86	2	US-09-461-325-456	Sequence 456, App
219	27	65.9	86	2	US-10-012-542-456	Sequence 456, App
220	27	65.9	86	2	US-10-115-123-456	Sequence 456, App
221	27	65.9	91	2	US-09-107-433-4174	Sequence 4174, Ap
222	27	65.9	91	2	US-09-813-290-7	Sequence 7, Appli
223	27	65.9	92	2	US-09-302-626B-36	Sequence 36, Appl
224	27	65.9	95	2	US-09-270-767-37620	Sequence 37620, A
225	27	65.9	95	2	US-09-270-767-52837	Sequence 52837, A
226	27	65.9	98	2	US-09-513-999C-4855	Sequence 4855, Ap
227	27	65.9	100	2	US-09-079-030-43	Sequence 43, Appl
228	27	65.9	103	2	US-09-302-626B-38	Sequence 38, Appl
229	27	65.9	113	2	US-09-710-279-2338	Sequence 2338, Ap
230	27	65.9	115	2	US-09-605-703B-310	Sequence 310, App
231	27	65.9	115	2	US-09-605-703B-312	Sequence 312, App
232	27	65.9	116	1	US-08-197-792-38	Sequence 38, Appl
233	27	65.9	116	1	US-08-459-850-38	Sequence 38, Appl
234	27	65.9	116	1	US-08-459-214-38	Sequence 38, Appl
235	27	65.9	123	2	US-09-270-767-42192	Sequence 42192, A
236	27	65.9	138	2	US-09-180-422B-12	Sequence 12, Appl
237	27	65.9	144	2	US-09-594-193-11	Sequence 11, Appl
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242	27	65.9	155	2	US-09-134-000C-4095	Sequence 4095, Ap
243	27	65.9	167	2	US-09-270-767-40583	Sequence 40583, A
244	27	65.9	167	2	US-09-270-767-55799	Sequence 55799, A
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247	27	65.9	176	2	US-09-732-210-1080	Sequence 1080, Ap
248	27	65.9	178	2	US-09-270-767-37772	Sequence 37772, A
249	27	65.9	178	2	US-09-270-767-52989	Sequence 52989, A
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253	27	65.9	191	2	US-09-107-433-3219	Sequence 3219, Ap
254	27	65.9	194	2	US-09-489-039A-14065	Sequence 14065, A
255	27	65.9	195	2	US-09-252-991A-25539	Sequence 25539, A
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258	27	65.9	225	2	US-09-489-847-238	Sequence 238, App
259	27	65.9	225	2	US-09-489-847-353	Sequence 353, App
260	27	65.9	227	2	US-09-270-767-46707	Sequence 46707, A
261	27	65.9	230	2	US-09-270-767-43372	Sequence 43372, A
262	27	65.9	236	1	US-08-684-862-4	Sequence 4, Appli
263	27	65.9	256	2	US-09-949-016-6707	Sequence 6707, Ap
264	27	65.9	259	2	US-09-477-135A-133	Sequence 133, App
265	27	65.9	282	2	US-09-328-352-8059	Sequence 8059, Ap
266	27	65.9	294	2	US-09-640-211A-669	Sequence 669, App
267	27	65.9	297	2	US-09-949-016-10529	Sequence 10529, A
268	27	65.9	300	2	US-09-461-774-6	Sequence 6, Appli
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274	27	65.9	364	1	US-08-459-850-29	Sequence 29, Appl
275	27	65.9	364	1	US-08-459-214-29	Sequence 29, Appl
276	27	65.9	379	2	US-09-270-767-42707	Sequence 42707, A
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279	27	65.9	409	2	US-09-252-991A-29674	Sequence 29674, A
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284	27	65.9	425	2	US-09-543-681A-7042	Sequence 7042, Ap
285	27	65.9	428	2	US-09-134-000C-6457	Sequence 6457, Ap
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289	27	65.9	441	4	PCT-US95-08071-98	Sequence 98, Appl
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304	27	65.9	556	1	US-08-453-274B-98	Sequence 98, Appl
305	27	65.9	556	1	US-08-453-695A-98	Sequence 98, Appl
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307	27	65.9	556	2	US-09-099-639-98	Sequence 98, Appl
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310	27	65.9	559	2	US-09-212-168-6	Sequence 6, Appli
311	27	65.9	559	2	US-09-854-549A-7	Sequence 7, Appli
312	27	65.9	563	2	US-09-949-016-6287	Sequence 6287, Ap
313	27	65.9	567	2	US-09-543-681A-6761	Sequence 6761, Ap
314	27	65.9	568	2	US-09-270-767-46388	Sequence 46388, A
315	27	65.9	576	2	US-09-248-796A-20509	Sequence 20509, A
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317	27	65.9	580	2	US-09-949-016-8642	Sequence 8642, Ap
318	27	65.9	613	2	US-09-270-767-45961	Sequence 45961, A
319	27	65.9	651	2	US-09-583-110-3943	Sequence 3943, Ap
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322	27	65.9	687	1	US-08-164-839-31	Sequence 31, Appl
323	27	65.9	687	1	US-08-164-839-33	Sequence 33, Appl
324	27	65.9	687	1	US-08-583-799-31	Sequence 31, Appl
325	27	65.9	687	1	US-08-583-799-33	Sequence 33, Appl
326	27	65.9	687	2	US-09-252-991A-26187	Sequence 26187, A
327	27	65.9	688	1	US-08-164-839-70	Sequence 70, Appl
328	27	65.9	688	1	US-08-164-839-72	Sequence 72, Appl
329	27	65.9	688	1	US-08-583-799-70	Sequence 70, Appl
330	27	65.9	688	1	US-08-583-799-72	Sequence 72, Appl
331	27	65.9	699	2	US-09-543-681A-5118	Sequence 5118, Ap
332	27	65.9	785	2	US-09-079-030-216	Sequence 216, App
333	27	65.9	793	1	US-08-720-484A-2	Sequence 2, Appli
334	27	65.9	793	2	US-08-953-823A-2	Sequence 2, Appli
335	27	65.9	793	2	US-09-293-505-16	Sequence 16, Appl
336	27	65.9	793	2	US-09-293-505-17	Sequence 17, Appl
337	27	65.9	793	2	US-09-398-239-2	Sequence 2, Appli
338	27	65.9	793	2	US-09-560-876A-2	Sequence 2, Appli
339	27	65.9	793	2	US-09-060-939A-16	Sequence 16, Appl
340	27	65.9	793	2	US-09-060-939A-17	Sequence 17, Appl
341	27	65.9	803	2	US-09-293-505-15	Sequence 15, Appl
342	27	65.9	803	2	US-09-060-939A-15	Sequence 15, Appl
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345	27	65.9	840	2	US-09-079-030-214	Sequence 214, App
346	27	65.9	883	2	US-09-543-681A-6947	Sequence 6947, Ap
347	27	65.9	906	2	US-09-417-039-11	Sequence 11, Appl
348	27	65.9	909	2	US-09-248-796A-16165	Sequence 16165, A
349	27	65.9	919	2	US-09-949-016-7873	Sequence 7873, Ap
350	27	65.9	937	2	US-09-538-092-980	Sequence 980, App
351	27	65.9	937	2	US-09-949-016-6054	Sequence 6054, Ap
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355	27	65.9	966	1	US-08-909-983-2	Sequence 2, Appli
356	27	65.9	975	2	US-09-328-352-4764	Sequence 4764, Ap
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358	27	65.9	1250	2	US-09-589-619-9	Sequence 9, Appli
359	27	65.9	1271	1	US-08-095-734-2	Sequence 2, Appli
360	27	65.9	1271	1	US-08-444-623-2	Sequence 2, Appli
361	27	65.9	1271	2	US-08-471-869-2	Sequence 2, Appli
362	27	65.9	1271	2	US-09-342-563-2	Sequence 2, Appli
363	27	65.9	1271	4	PCT-US94-08267-2	Sequence 2, Appli
364	27	65.9	1356	2	US-09-487-558B-306	Sequence 306, App
365	27	65.9	1626	1	US-08-771-602D-2	Sequence 2, Appli
366	27	65.9	1626	2	US-09-232-446B-2	Sequence 2, Appli
367	27	65.9	2322	2	US-09-976-594-15	Sequence 15, Appl
368	27	65.9	2322	2	US-09-919-039-15	Sequence 15, Appl
369	27	65.9	2442	2	US-09-514-247A-10	Sequence 10, Appl
370	27	65.9	2442	2	US-09-538-092-1370	Sequence 1370, Ap
371	27	65.9	3025	6	5223423-3	Patent No. 5223423
372	27	65.9	4536	2	US-09-180-422B-27	Sequence 27, Appl
373	27	65.9	4536	2	US-09-079-030-1	Sequence 1, Appli
374	27	65.9	4563	2	US-09-108-006C-1	Sequence 1, Appli
375	27	65.9	4563	2	US-09-538-092-842	Sequence 842, App
376	26.5	64.6	307	2	US-09-489-039A-14128	Sequence 14128, A
377	26.5	64.6	320	2	US-09-489-039A-8016	Sequence 8016, Ap
378	26.5	64.6	1838	2	US-09-270-767-45188	Sequence 45188, A
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380	26	63.4	19	1	US-08-854-768-7	Sequence 7, Appli
381	26	63.4	19	1	US-08-737-045-7	Sequence 7, Appli
382	26	63.4	25	2	US-09-429-801-15	Sequence 15, Appl
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384	26	63.4	44	1	US-08-854-768-4	Sequence 4, Appli
385	26	63.4	44	1	US-08-737-045-4	Sequence 4, Appli
386	26	63.4	51	2	US-09-439-410A-97	Sequence 97, Appl
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388	26	63.4	70	2	US-09-252-991A-22069	Sequence 22069, A
389	26	63.4	70	2	US-09-248-796A-24176	Sequence 24176, A
390	26	63.4	75	2	US-09-902-540-12923	Sequence 12923, A
391	26	63.4	76	2	US-09-134-001C-3470	Sequence 3470, Ap
392	26	63.4	76	2	US-09-513-999C-7632	Sequence 7632, Ap
393	26	63.4	79	2	US-09-543-681A-4799	Sequence 4799, Ap
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395	26	63.4	84	2	US-09-107-433-4525	Sequence 4525, Ap
396	26	63.4	85	2	US-09-247-155-123	Sequence 123, App
397	26	63.4	85	2	US-09-621-976-5559	Sequence 5559, Ap
398	26	63.4	85	2	US-09-903-190-123	Sequence 123, App
399	26	63.4	90	2	US-09-107-532A-4618	Sequence 4618, Ap
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401	26	63.4	95	2	US-09-263-810-6	Sequence 6, Appli
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403	26	63.4	95	2	US-09-471-276-1555	Sequence 1555, Ap
404	26	63.4	95	2	US-09-985-911-6	Sequence 6, Appli
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406	26	63.4	107	2	US-09-489-039A-8794	Sequence 8794, Ap
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409	26	63.4	108	2	US-09-763-620-4	Sequence 4, Appli
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416	26	63.4	128	2	US-09-252-991A-25933	Sequence 25933, A
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419	26	63.4	132	2	US-09-164-615-50	Sequence 50, Appl
420	26	63.4	132	2	US-09-164-615-51	Sequence 51, Appl
421	26	63.4	132	2	US-09-164-615-52	Sequence 52, Appl
422	26	63.4	132	2	US-09-164-615-53	Sequence 53, Appl
423	26	63.4	132	2	US-09-164-615-54	Sequence 54, Appl
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432	26	63.4	149	2	US-09-270-767-46053	Sequence 46053, A
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443	26	63.4	178	2	US-09-248-796A-14165	Sequence 14165, A
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445	26	63.4	181	2	US-09-902-540-14373	Sequence 14373, A
446	26	63.4	182	2	US-09-252-991A-28591	Sequence 28591, A
447	26	63.4	182	2	US-09-489-039A-8960	Sequence 8960, Ap
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452	26	63.4	192	2	US-09-439-410A-52	Sequence 52, Appl
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472	26	63.4	218	1	US-08-448-873-34	Sequence 34, Appl
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519	26	63.4	296	2	US-09-248-796A-25639	Sequence 25639, A
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585	26	63.4	397	2	US-09-088-216-6	Sequence 6, Appli
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691	26	63.4	707	2	US-09-228-986-80	Sequence 80, Appl
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704	26	63.4	732	2	US-10-116-260-43	Sequence 43, Appl
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706	26	63.4	732	2	US-10-115-695-43	Sequence 43, Appl
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717	26	63.4	769	2	US-09-854-856-44	Sequence 44, Appl
718	26	63.4	769	2	US-09-540-236-2782	Sequence 2782, Ap
719	26	63.4	769	2	US-10-010-720-44	Sequence 44, Appl
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721	26	63.4	780	1	US-08-973-831-2	Sequence 2, Appli
722	26	63.4	780	4	PCT-US96-09530A-2	Sequence 2, Appli
723	26	63.4	782	2	US-09-710-279-2352	Sequence 2352, Ap
724	26	63.4	794	2	US-09-088-216-10	Sequence 10, Appl
725	26	63.4	794	2	US-09-134-001C-4310	Sequence 4310, Ap
726	26	63.4	800	2	US-09-328-352-7036	Sequence 7036, Ap
727	26	63.4	801	2	US-09-854-856-28	Sequence 28, Appl
728	26	63.4	801	2	US-10-010-720-28	Sequence 28, Appl
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731	26	63.4	815	2	US-09-196-270-7	Sequence 7, Appli
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733	26	63.4	829	2	US-10-010-720-12	Sequence 12, Appl
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739	26	63.4	890	2	US-08-170-558-2	Sequence 2, Appli
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743	26	63.4	892	2	US-09-328-352-8164	Sequence 8164, Ap
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747	26	63.4	902	1	US-08-818-823-6	Sequence 6, Appli
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764	26	63.4	982	2	US-10-010-720-6	Sequence 6, Appli
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778	26	63.4	1151	2	US-09-023-905A-4	Sequence 4, Appli
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842	26	63.4	2141	2	US-09-854-856-56	Sequence 56, Appl
843	26	63.4	2141	2	US-10-010-720-56	Sequence 56, Appl
844	26	63.4	2157	2	US-09-854-856-52	Sequence 52, Appl
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847	26	63.4	2169	2	US-10-010-720-40	Sequence 40, Appl
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856	26	63.4	2229	2	US-10-010-720-8	Sequence 8, Appli
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858	26	63.4	2245	2	US-10-010-720-4	Sequence 4, Appli
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860	26	63.4	2294	2	US-10-010-720-50	Sequence 50, Appl
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862	26	63.4	2318	2	US-09-660-541-24	Sequence 24, Appl
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864	26	63.4	2322	2	US-10-010-720-34	Sequence 34, Appl
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866	26	63.4	2354	2	US-10-010-720-18	Sequence 18, Appl

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872	26	63.4	2396	2	US-10-226-065-2	Sequence 2, Appli
873	26	63.4	2441	1	US-08-194-468-2	Sequence 2, Appli
874	26	63.4	2441	2	US-08-961-739-2	Sequence 2, Appli
875	26	63.4	2441	2	US-09-514-247A-8	Sequence 8, Appli
876	26	63.4	2441	2	US-09-686-316-2	Sequence 2, Appli
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879	26	63.4	2627	1	US-09-060-836-3	Sequence 3, Appli
880	26	63.4	2627	2	US-09-184-445-3	Sequence 3, Appli
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883	26	63.4	2710	2	US-09-210-288-12	Sequence 12, Appl
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894	25	61.0	20	2	US-09-743-533-15	Sequence 15, Appl
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898	25	61.0	62	2	US-09-513-999C-7695	Sequence 7695, Ap
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907	25	61.0	66	2	US-09-011-356-31	Sequence 31, Appl
908	25	61.0	66	2	US-09-201-932-31	Sequence 31, Appl
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921	25	61.0	100	2	US-10-104-047-3175	Sequence 3175, Ap
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927	25	61.0	106	2	US-09-710-279-178	Sequence 178, App
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933	25	61.0	109	2	US-09-134-001C-4896	Sequence 4896, Ap
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983	25	61.0	170	2	US-09-270-767-34481	Sequence 34481, A
984	25	61.0	170	2	US-09-270-767-49698	Sequence 49698, A
985	25	61.0	172	1	US-08-812-645-1	Sequence 1, Appli
986	25	61.0	172	2	US-09-543-681A-5395	Sequence 5395, Ap
987	25	61.0	173	2	US-09-252-991A-31983	Sequence 31983, A
988	25	61.0	173	2	US-09-949-016-9085	Sequence 9085, Ap
989	25	61.0	174	2	US-09-252-991A-31072	Sequence 31072, A
990	25	61.0	174	2	US-09-270-767-61801	Sequence 61801, A
991	25	61.0	174	2	US-10-104-047-2183	Sequence 2183, Ap
992	25	61.0	175	2	US-09-270-767-35461	Sequence 35461, A
993	25	61.0	175	2	US-09-270-767-50678	Sequence 50678, A
994	25	61.0	176	2	US-09-270-767-57508	Sequence 57508, A
995	25	61.0	178	2	US-09-248-796A-16561	Sequence 16561, A
996	25	61.0	179	2	US-09-198-452A-304	Sequence 304, App
997	25	61.0	179	2	US-09-438-185A-293	Sequence 293, App
998	25	61.0	182	2	US-09-673-395A-192	Sequence 192, App
999	25	61.0	183	2	US-09-270-767-40388	Sequence 40388, A
1000	25	61.0	183	2	US-09-270-767-55604	Sequence 55604, A

ALIGNMENTS

RESULT 1

US-09-187-330-6

```

; Sequence 6, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III-8
;   OTHER INFORMATION: active site core peptide, clone 25 sequence (NAP)
US-09-187-330-6

```

Query Match 100.0%; Score 41; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 2

US-09-267-511-2

; Sequence 2, Application US/09267511

; Patent No. 6933277

; GENERAL INFORMATION:

; APPLICANT: Brenneman, Douglas E.

; APPLICANT: Spong, Catherine Y.

; APPLICANT: Gozes, Illana

; APPLICANT: Bassan, Merav

; APPLICANT: Zamostiano, Rachel

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; APPLICANT: Ramot University Authority for Applied Research

; APPLICANT: and Industrial Development, Ltd.

; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell

; TITLE OF INVENTION: Death With ADNF Polypeptides

; FILE REFERENCE: 015280-377000US

; CURRENT APPLICATION NUMBER: US/09/267,511

; CURRENT FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:activity

; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)

; OTHER INFORMATION: active site

US-09-267-511-2

Query Match 100.0%; Score 41; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 3

US-09-187-330-33

; Sequence 33, Application US/09187330

; Patent No. 6613740

; GENERAL INFORMATION:

; APPLICANT: Gozes, Illana

; APPLICANT: Brenneman, Douglas E.

; APPLICANT: Bassan, Merav

```

; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-187-330-33

```

```

Query Match          100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      3 NAPVSIPQ 10

```

RESULT 4

US-09-267-511-23

```

; Sequence 23, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 10
;   TYPE: PRT

```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-23

Query Match 100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 3 NAPVSIPQ 10

RESULT 5

US-09-187-330-34

; Sequence 34, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-187-330-34

Query Match 100.0%; Score 41; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 4 NAPVSIPQ 11

RESULT 6

US-09-267-511-24

```

; Sequence 24, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-267-511-24

```

```

Query Match          100.0%;  Score 41;  DB 2;  Length 13;
Best Local Similarity 100.0%;  Pred. No. 0.16;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      4 NAPVSIPQ 11

```

RESULT 7

```

US-09-187-330-35
; Sequence 35, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485

```

; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-187-330-35

Query Match 100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 8

US-09-267-511-25

; Sequence 25, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-25

Query Match 100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

Db

|||||||
6 NAPVSIPQ 13

RESULT 9

US-09-267-511-19

; Sequence 19, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-19

Query Match 100.0%; Score 41; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||||
Db 6 NAPVSIPQ 13

RESULT 10

US-09-267-511-26

; Sequence 26, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services

```

; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-267-511-26

```

```

Query Match          100.0%; Score 41; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches      8; Conservative    0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      8 NAPVSIPQ 15

```

RESULT 11

```

US-09-187-330-12
; Sequence 12, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-187-330-12

```

Query Match 100.0%; Score 41; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 9 NAPVSIPQ 16

RESULT 12

US-09-267-511-18

; Sequence 18, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide

US-09-267-511-18

Query Match 100.0%; Score 41; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 13

US-09-267-511-20

; Sequence 20, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.

```
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-267-511-20
```

```
Query Match          100.0%; Score 41; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches      8; Conservative    0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      6 NAPVSIPQ 13
```

RESULT 14

```
US-09-187-330-10
; Sequence 10, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 88
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may be
; OTHER INFORMATION: present or absent
US-09-187-330-10

```

```

Query Match          100.0%; Score 41; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      41 NAPVSIPQ 48

```

RESULT 15

US-09-267-511-4

```

; Sequence 4, Application US/09267511
; Patent No. 6933277
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
; FEATURE:

```



```

; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may
; OTHER INFORMATION: be present or absent
US-09-267-511-4

```

```

Query Match          100.0%; Score 41; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      41 NAPVSIPQ 48

```

RESULT 16

```

US-09-187-330-57
; Sequence 57, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-330-57

```

```

Query Match          100.0%; Score 41; DB 2; Length 726;
Best Local Similarity 100.0%; Pred. No. 12;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      59 NAPVSIPQ 66

```

RESULT 17

US-09-187-330-32

```
; Sequence 32, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 781
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human activity dependent neurotrophic factor III
;   OTHER INFORMATION: (ADNF III)
```

US-09-187-330-32

```
Query Match          100.0%; Score 41; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 13;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      33 NAPVSIPQ 40
```

RESULT 18

US-09-187-330-31

```
; Sequence 31, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
```

```

; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 787
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: mouse activity dependent neurotrophic factor III
;   OTHER INFORMATION: (ADNF III)
US-09-187-330-31

```

```

Query Match          100.0%; Score 41; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 13;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      33 NAPVSIPQ 40

```

RESULT 19

```

US-09-187-330-41
; Sequence 41, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 800
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(800)
;   OTHER INFORMATION: translation of H3' human ADNF III cDNA clone
US-09-187-330-41

```

```

Query Match          100.0%; Score 41; DB 2; Length 800;
Best Local Similarity 100.0%; Pred. No. 13;

```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 52 NAPVSIPQ 59

RESULT 20

US-09-187-330-3

; Sequence 3, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III) cDNA clone
US-09-187-330-3

Query Match 100.0%; Score 41; DB 2; Length 806;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 52 NAPVSIPQ 59

RESULT 21

US-09-187-330-55

; Sequence 55, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America

```
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
;   LENGTH: 828
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-187-330-55
```

```
Query Match          100.0%;  Score 41;  DB 2;  Length 828;
Best Local Similarity 100.0%;  Pred. No. 13;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      74 NAPVSIPQ 81
```

RESULT 22

```
US-09-187-330-59
; Sequence 59, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
;   LENGTH: 874
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-187-330-59
```

```
Query Match          100.0%;  Score 41;  DB 2;  Length 874;
Best Local Similarity 100.0%;  Pred. No. 14;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 126 NAPVSIPQ 133

RESULT 23

US-09-187-330-1

; Sequence 1, Application US/09187330

; Patent No. 6613740

; GENERAL INFORMATION:

; APPLICANT: Gozes, Illana

; APPLICANT: Brenneman, Douglas E.

; APPLICANT: Bassan, Merav

; APPLICANT: Zamostiano, Rachel

; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)

; FILE REFERENCE: 015280-291200US

; CURRENT APPLICATION NUMBER: US/09/187,330

; CURRENT FILING DATE: 1998-11-06

; EARLIER APPLICATION NUMBER: US 60/037,404

; EARLIER FILING DATE: 1997-02-07

; EARLIER APPLICATION NUMBER: WO PCT/US98/02485

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1000

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: H3' human activity dependent neurotrophic factor

; OTHER INFORMATION: III (ADNF III) clone

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (801)

; OTHER INFORMATION: Xaa = unknown

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (817)

; OTHER INFORMATION: Xaa = unknown

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (821)

; OTHER INFORMATION: Xaa = unknown

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (833)

; OTHER INFORMATION: Xaa = unknown

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (854)

; OTHER INFORMATION: Xaa = unknown

; FEATURE:

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; NAME/KEY: MOD_RES
; LOCATION: (866)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (870)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (877)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (882)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (922)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (948)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (959)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (964)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (967)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (980)
; OTHER INFORMATION: Xaa = unknown
US-09-187-330-1

```

```

Query Match          100.0%; Score 41; DB 2; Length 1000;
Best Local Similarity 100.0%; Pred. No. 16;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          1 NAPVSIPQ 8
             |||||
Db          52 NAPVSIPQ 59

```

```

RESULT 24
US-09-364-609-8
; Sequence 8, Application US/09364609A
; Patent No. 6649411
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.

```

```

; APPLICANT: Zamostiano, Rachel
; APPLICANT: Gelber, Edgar
; APPLICANT: Pinhasov, Albert
; APPLICANT: Bassan, Merav
; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells With ADNF III
; TITLE OF INVENTION: Antisense Oligonucleotides
; FILE REFERENCE: 019856-000100US
; CURRENT APPLICATION NUMBER: US/09/364,609A
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1102
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human activity dependent neurotrophic factor III
;   OTHER INFORMATION: (ADNF III) cDNA
US-09-364-609-8

```

```

Query Match          100.0%; Score 41; DB 2; Length 1102;
Best Local Similarity 100.0%; Pred. No. 18;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

QY          1 NAPVSIPQ 8
             |||||
Db          354 NAPVSIPQ 361

```

RESULT 25

```

US-09-187-330-28
; Sequence 28, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence

```


; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sequence of p25
; OTHER INFORMATION: clone with structural similarity to active peptide
; OTHER INFORMATION: of ADNF I
US-09-187-330-28

Query Match 87.8%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||
Db 3 NAPVSIP 9

RESULT 26

US-09-252-991A-31993
; Sequence 31993, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31993
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31993

Query Match 87.8%; Score 36; DB 2; Length 360;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 285 NAPVSYQ 292

RESULT 27

US-09-634-238-237
; Sequence 237, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James

; APPLICANT: Christensson, Anna C.
 ; APPLICANT: Holland, Ross
 ; APPLICANT: O'Toole, Paul W.
 ; APPLICANT: Reid, Julian R.
 ; APPLICANT: Coolbear, Timothy
 ; TITLE OF INVENTION: Polynucleotides, materials incorporating
 ; TITLE OF INVENTION: them and methods for using them.
 ; FILE REFERENCE: 11000.1043U1
 ; CURRENT APPLICATION NUMBER: US/09/634,238
 ; CURRENT FILING DATE: 2000-08-08
 ; NUMBER OF SEQ ID NOS: 422
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 237
 ; LENGTH: 510
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus rhamnosus
 US-09-634-238-237

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | | : | | |
 Db 215 NTPISIPQ 222

RESULT 28

US-10-169-048-18
 ; Sequence 18, Application US/10169048
 ; Patent No. 6951732
 ; GENERAL INFORMATION:
 ; APPLICANT: Clarke, Edna Elizabeth
 ; APPLICANT: Zhou, Liqing
 ; APPLICANT: Shea, Jacqueline Elizabeth
 ; APPLICANT: Feldman, Robert Graham
 ; APPLICANT: Holden, David William
 ; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And
 Their Use
 ; FILE REFERENCE: GJE-97
 ; CURRENT APPLICATION NUMBER: US/10/169,048
 ; CURRENT FILING DATE: 2002-06-24
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04997
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 510
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pyogenes
 US-10-169-048-18

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

Db | |:||||
215 NTPISIPQ 222

RESULT 29

US-09-134-000C-6226
; Sequence 6226, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6226
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6226

Query Match 87.8%; Score 36; DB 2; Length 519;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | |:||||
Db 224 NTPISIPQ 231

RESULT 30

US-09-328-352-4822
; Sequence 4822, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4822
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4822

Query Match 82.9%; Score 34; DB 2; Length 469;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|:
Db 76 NAPISVP 82

RESULT 31

US-09-949-016-9522
; Sequence 9522, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9522
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9522

Query Match 82.9%; Score 34; DB 2; Length 849;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| ||:|
Db 768 NGPVTIPQ 775

RESULT 32

US-09-489-039A-7548
; Sequence 7548, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7548
; LENGTH: 205

; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7548

Query Match 80.5%; Score 33; DB 2; Length 205;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||: ||
Db 64 NAPVATPQ 71

RESULT 33

US-09-808-387-20
; Sequence 20, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 295
; TYPE: PRT
; ORGANISM: rat
US-09-808-387-20

Query Match 80.5%; Score 33; DB 2; Length 295;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:
Db 221 NSPVSLPE 228

RESULT 34

US-09-808-387-12
; Sequence 12, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mouse
US-09-808-387-12

Query Match 80.5%; Score 33; DB 2; Length 344;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
|:|:|:|:
Db 270 NSPVSLPE 277

RESULT 35

US-09-808-387-18
; Sequence 18, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 344
; TYPE: PRT
; ORGANISM: rat
US-09-808-387-18

Query Match 80.5%; Score 33; DB 2; Length 344;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
|:|:|:|:
Db 270 NSPVSLPE 277

RESULT 36

US-09-808-387-6
; Sequence 6, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A

; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-808-387-6

Query Match 80.5%; Score 33; DB 2; Length 386;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 312 NSPVSLPE 319

RESULT 37

US-09-489-039A-9148
; Sequence 9148, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9148
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9148

Query Match 80.5%; Score 33; DB 2; Length 481;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 352 NLPVAIPQ 359

RESULT 38

US-09-808-387-4
; Sequence 4, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research

; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-808-387-4

Query Match 80.5%; Score 33; DB 2; Length 557;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 483 NSPVSLPE 490

RESULT 39

US-09-808-387-10
; Sequence 10, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 557
; TYPE: PRT
; ORGANISM: mouse
US-09-808-387-10

Query Match 80.5%; Score 33; DB 2; Length 557;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 483 NSPVSLPE 490

RESULT 40

US-09-808-387-2
; Sequence 2, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:

; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-808-387-2

Query Match 80.5%; Score 33; DB 2; Length 574;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 500 NSPVSLPE 507

RESULT 41

US-09-808-387-8
; Sequence 8, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 574
; TYPE: PRT
; ORGANISM: mouse
US-09-808-387-8

Query Match 80.5%; Score 33; DB 2; Length 574;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 500 NSPVSLPE 507

RESULT 42

US-09-808-387-16

```
; Sequence 16, Application US/09808387
; Patent No. 6962985
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: CeMines Research
; TITLE OF INVENTION: MAMMALIAN NEURALIZED FAMILY OF
; TITLE OF INVENTION: TRANSCRIPTION REGULATORS AND USES THEREFOR
; FILE REFERENCE: CEMRES.001A
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 574
; TYPE: PRT
; ORGANISM: rat
US-09-808-387-16
```

```
Query Match          80.5%; Score 33; DB 2; Length 574;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches      5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 NAPVSIPQ 8
        |:|:|:|:|:
Db      500 NSPVSLPE 507
```

RESULT 43

```
US-09-270-767-33696
; Sequence 33696, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33696
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-33696
```

```
Query Match          75.6%; Score 31; DB 2; Length 114;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches      5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 NAPVSIPQ 8
        |||:| |:
Db      107 NAPISTPR 114
```

RESULT 44

US-09-270-767-48913

; Sequence 48913, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 48913
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-48913

Query Match 75.6%; Score 31; DB 2; Length 114;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||:| |:
 Db 107 NAPISTPR 114

RESULT 45

US-09-328-352-8057

; Sequence 8057, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 8057
 ; LENGTH: 292
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-8057

Query Match 75.6%; Score 31; DB 2; Length 292;
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | |::||
 Db 21 NTPIALPQ 28

RESULT 46

US-09-248-796A-24473

; Sequence 24473, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA
 ALBICANS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 24473
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-24473

Query Match 75.6%; Score 31; DB 2; Length 306;
 Best Local Similarity 62.5%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | | | : | |
 Db 47 NLPTSV PQ 54

RESULT 47

US-09-543-681A-4789

; Sequence 4789, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS
 MIRABILIS FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 4789
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-4789

Query Match 75.6%; Score 31; DB 2; Length 317;
 Best Local Similarity 75.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||:| ||
Db 69 NAPLSDPQ 76

RESULT 48

US-09-489-039A-7535
; Sequence 7535, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7535
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7535

Query Match 75.6%; Score 31; DB 2; Length 376;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|| :|:|
Db 88 NAQISVPQ 95

RESULT 49

US-09-600-099-6
; Sequence 6, Application US/09600099
; Patent No. 6649382
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang Yuo
; APPLICANT: CHOI, Jong-il
; APPLICANT: CHOO, Seung-Ho
; APPLICANT: YOON, Hye-Sung
; APPLICANT: HAN, Kyuboem
; APPLICANT: SONG, Ji-Yong
; APPLICANT: LEE, Yong-Hyun
; APPLICANT: HUH, Tae-Lin
; APPLICANT: HONG, Sung-Kook
; TITLE OF INVENTION: POLYHYDROXYALKANOATE BIOSYNTHESIS-RELATED GENES DERIVED FROM Alca
; TITLE OF INVENTION: ligenes latus
; FILE REFERENCE: 428.1001
; CURRENT APPLICATION NUMBER: US/09/600,099
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: KR 98-1422
; PRIOR FILING DATE: 1998-01-19

; PRIOR APPLICATION NUMBER: KR 98-1423
; PRIOR FILING DATE: 1998-01-19
; PRIOR APPLICATION NUMBER: KR 98-58760
; PRIOR FILING DATE: 1998-12-26
; PRIOR APPLICATION NUMBER: PCT/KR99/00031
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: KOPATIN 1.5
; SEQ ID NO 6
; LENGTH: 392
; TYPE: PRT
; ORGANISM: *Alcaligenes latus*
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(392)
; OTHER INFORMATION: beta-ketothiolase
US-09-600-099-6

Query Match 75.6%; Score 31; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|||
Db 201 PVSIPQ 206

RESULT 50

US-09-902-540-12378
; Sequence 12378, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12378
; LENGTH: 444
; TYPE: PRT
; ORGANISM: *Myxococcus xanthus*
US-09-902-540-12378

Query Match 75.6%; Score 31; DB 2; Length 444;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||
Db 18 NAPVMIP 24

Search completed: April 26, 2006, 00:23:45
Job time : 59 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 00:18:47 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-10-748-765-2
Perfect score: 41
Sequence: 1 NAPVSIPQ 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	1005	2	T12546	hypothetical prote
2	36	87.8	631	2	B83404	hypothetical prote
3	35	85.4	299	2	D95412	hypothetical prote
4	34	82.9	136	2	G69440	conserved hypothet
5	34	82.9	1272	2	T30248	fragile X mental r
6	33	80.5	198	2	AI0632	trp repressor bind
7	33	80.5	467	2	AH0813	probable ethanolam
8	33	80.5	479	2	H86465	F12G12.1 protein -
9	33	80.5	601	2	S47896	probable molybdopt
10	33	80.5	1119	2	T50995	related to cytoske
11	33	80.5	1213	2	S16356	ovo protein - frui
12	33	80.5	2251	2	T24490	hypothetical prote
13	32	78.0	97	2	T25754	hypothetical prote

14	32	78.0	249	2	AE1928	hypothetical prote
15	32	78.0	301	2	AE0243	hypothetical prote
16	32	78.0	400	2	T47111	probable acetyl-Co
17	32	78.0	657	2	F97604	hypothetical prote
18	32	78.0	668	2	AH2826	conserved hypothet
19	32	78.0	1017	2	B70985	probable polyketid
20	32	78.0	2774	2	A43359	microtubule-associ
21	31	75.6	159	2	C81662	cytosolic acyl-CoA
22	31	75.6	263	2	C83959	ribonuclease H rnh
23	31	75.6	341	2	T35027	hypothetical prote
24	31	75.6	350	2	AE0637	conserved hypothet
25	31	75.6	358	2	B81194	conserved hypothet
26	31	75.6	358	2	A81831	hypothetical prote
27	31	75.6	392	2	T51772	acetyl-CoA C-acety
28	31	75.6	393	2	C89801	hypothetical prote
29	31	75.6	393	2	S72804	acetyl-CoA C-acety
30	31	75.6	394	2	B48376	acetyl-CoA C-acety
31	31	75.6	395	2	AG2606	conserved hypothet
32	31	75.6	395	2	F97388	probable lipase (A
33	31	75.6	424	2	T14728	probable betaine-a
34	31	75.6	459	2	D34791	interleukin-7 rece
35	31	75.6	504	2	T16526	hypothetical prote
36	31	75.6	518	2	F89888	conserved hypothet
37	31	75.6	558	1	B28392	penicillin amidase
38	31	75.6	558	2	S27199	cephalosporin acyl
39	31	75.6	679	2	T52163	hypothetical prote
40	31	75.6	787	2	T41974	replication origin
41	31	75.6	881	1	RGBYG4	regulatory protein
42	31	75.6	936	2	S57637	hexon protein - hu
43	31	75.6	952	1	HXAD5	hexon protein - hu
44	31	75.6	967	1	HXAD2	hexon protein - hu
45	31	75.6	2512	2	E70751	probable nrp prote
46	31	75.6	3839	2	T49799	related to TOM1 pr
47	30	73.2	26	2	S06675	apidaecin Ib precu
48	30	73.2	101	2	AE0106	conserved hypothet
49	30	73.2	104	2	A22706	vitelline membrane
50	30	73.2	133	2	F64700	biopolymer transpo
51	30	73.2	144	2	S35331	apidaecin 22 precu
52	30	73.2	154	2	T19903	hypothetical prote
53	30	73.2	160	2	F71502	probable acyl-coa
54	30	73.2	163	2	T18424	hypothetical prote
55	30	73.2	168	2	S35330	apidaecin 14 precu
56	30	73.2	183	2	S76453	hypothetical prote
57	30	73.2	184	2	E87506	hypothetical prote
58	30	73.2	192	2	T17331	hypothetical prote
59	30	73.2	200	2	H98209	hypothetical prote
60	30	73.2	200	2	AI3076	conserved hypothet
61	30	73.2	200	2	C95315	hypothetical prote
62	30	73.2	217	2	AI2567	hypothetical prote
63	30	73.2	219	2	E84117	hypothetical prote
64	30	73.2	244	2	E84885	hypothetical prote
65	30	73.2	254	2	AH2681	transcription regu
66	30	73.2	272	2	AB2625	conserved hypothet
67	30	73.2	272	2	A97407	hypothetical prote
68	30	73.2	283	2	S35332	apidaecin 73 precu
69	30	73.2	284	2	T20149	hypothetical prote
70	30	73.2	284	2	T14753	hypothetical prote

71	30	73.2	285	2	E84766	probable AT-hook D
72	30	73.2	288	2	B84829	hypothetical prote
73	30	73.2	298	2	F97463	probable lysR-like
74	30	73.2	300	2	S64995	probable spermidin
75	30	73.2	308	2	AH2896	transcription regu
76	30	73.2	308	2	B97672	rok family protein
77	30	73.2	322	2	S73795	hypothetical prote
78	30	73.2	330	2	AI2820	two component sens
79	30	73.2	331	2	AE3372	toluene tolerance
80	30	73.2	342	2	A97599	sensor histidine k
81	30	73.2	367	1	S24411	dual specificity p
82	30	73.2	367	1	S29090	dual specificity p
83	30	73.2	367	2	S52265	dual specificity p
84	30	73.2	411	2	E71873	hypothetical prote
85	30	73.2	488	2	A53572	prostaglandin E2 r
86	30	73.2	488	2	JC2241	prostaglandin E re
87	30	73.2	513	2	A46638	prostaglandin E re
88	30	73.2	516	2	T02189	hypothetical prote
89	30	73.2	552	2	G64957	flagellar basal-bo
90	30	73.2	552	2	E90963	flagellar hook-bas
91	30	73.2	552	2	E85811	flagellar hook-bas
92	30	73.2	565	2	E91268	thiol disulfide in
93	30	73.2	565	2	C86109	thiol disulfide in
94	30	73.2	565	2	S56364	inner membrane cop
95	30	73.2	570	2	AD0223	flagellar M-ring p
96	30	73.2	572	2	AB2708	penicillin-binding
97	30	73.2	593	2	C97490	penicillin binding
98	30	73.2	634	2	T18711	hypothetical prote
99	30	73.2	634	2	T18702	hypothetical prote
100	30	73.2	634	2	AD2343	hypothetical prote
101	30	73.2	638	2	T44763	conserved hypothet
102	30	73.2	674	1	A41670	carbon-monoxide de
103	30	73.2	676	2	S40939	hypothetical prote
104	30	73.2	681	2	S73550	DNA polymerase III
105	30	73.2	722	1	VCPVV2	coat protein VP1 -
106	30	73.2	780	2	T00366	hypothetical prote
107	30	73.2	814	2	S51451	probable membrane
108	30	73.2	821	2	S39983	eps8 protein - mou
109	30	73.2	829	1	IJHUCP	cadherin 3 precurs
110	30	73.2	855	2	T41336	probable nitrogen
111	30	73.2	861	2	E97473	1708 [imported] -
112	30	73.2	861	2	AI2691	copper transportin
113	30	73.2	868	2	S64747	probable membrane
114	30	73.2	869	2	H83500	probable glucosyl
115	30	73.2	889	2	AD2215	two-component hybr
116	30	73.2	926	2	AG1860	hypothetical prote
117	30	73.2	937	2	S55504	hexon protein - hu
118	30	73.2	937	2	S39301	hexon protein - hu
119	30	73.2	940	2	S37216	hexon protein - hu
120	30	73.2	942	2	S39298	hexon protein - hu
121	30	73.2	946	2	T16297	hypothetical prote
122	30	73.2	1001	2	T16419	hypothetical prote
123	30	73.2	1007	2	C84668	probable receptor-
124	30	73.2	1165	2	T16420	hypothetical prote
125	30	73.2	1167	2	B75258	probable S-layer p
126	30	73.2	1218	2	JS0069	hypothetical P1 op
127	30	73.2	1226	2	AB3327	hypothetical membr

128	30	73.2	1319	2	S49951	SSM4 protein - yea
129	30	73.2	1330	2	H89567	protein T08A9.1 [i
130	30	73.2	2938	2	T30249	cell proliferation
131	29	70.7	110	2	G72765	hypothetical prote
132	29	70.7	124	2	E84613	hypothetical prote
133	29	70.7	175	2	A97742	cytochrome c [impo
134	29	70.7	177	2	S34658	fimbrial protein F
135	29	70.7	180	2	G64661	ATP synthase F1, s
136	29	70.7	180	2	G71855	probable ATP synth
137	29	70.7	187	1	YQECKS	KS71A fimbrial pro
138	29	70.7	187	2	C43597	pilin type F7-1 pr
139	29	70.7	196	2	D75137	hypothetical prote
140	29	70.7	227	2	F64657	probable glucose-6
141	29	70.7	227	2	G71859	probable dehydroge
142	29	70.7	229	2	G70073	two-component resp
143	29	70.7	238	1	TRWV5Y	trypsin-like prote
144	29	70.7	241	2	JU0042	hypothetical 26.8K
145	29	70.7	247	2	AF3368	alanine-tRNA ligas
146	29	70.7	262	2	C83064	probable pili asse
147	29	70.7	276	2	T47734	hypothetical prote
148	29	70.7	285	2	S20853	glutenin low molec
149	29	70.7	286	2	T22444	hypothetical prote
150	29	70.7	304	2	T24703	hypothetical prote
151	29	70.7	306	2	AD1914	hypothetical prote
152	29	70.7	307	2	E82383	transcription regu
153	29	70.7	323	2	T52640	nuclease (EC 3.1.-
154	29	70.7	325	2	H90204	hypothetical prote
155	29	70.7	333	2	AI2473	oxidoreductase all
156	29	70.7	386	2	H75287	hypothetical prote
157	29	70.7	393	2	T20268	hypothetical prote
158	29	70.7	395	1	I50376	homeotic protein 1
159	29	70.7	395	1	S38821	homeotic protein 1
160	29	70.7	397	2	T40539	zinc finger protei
161	29	70.7	426	2	B71408	probable acylamino
162	29	70.7	432	2	T43476	hypothetical prote
163	29	70.7	471	2	S24339	H+-transporting tw
164	29	70.7	519	2	T23739	hypothetical prote
165	29	70.7	522	2	A84606	hypothetical prote
166	29	70.7	533	2	A33111	segmentation prote
167	29	70.7	560	2	S27874	steroid hormone re
168	29	70.7	568	2	G02753	testis specific ba
169	29	70.7	573	1	C64131	acetolactate synth
170	29	70.7	599	2	AD3017	hypothetical prote
171	29	70.7	599	2	D98267	ABC transporter AT
172	29	70.7	613	2	T47975	auxin response fac
173	29	70.7	728	2	T51071	related to trfA pr
174	29	70.7	742	2	T43520	condensin complex
175	29	70.7	755	2	B95342	NosR Regulatory pr
176	29	70.7	764	2	JC8016	acylaminoacyl-pept
177	29	70.7	770	2	T15742	hypothetical prote
178	29	70.7	807	2	B71605	hypothetical prote
179	29	70.7	867	1	GNLJSA	pol polyprotein -
180	29	70.7	867	1	GNLJMP	pol polyprotein (c
181	29	70.7	979	2	F81837	probable type III
182	29	70.7	979	2	G81103	type III restricti
183	29	70.7	1019	2	A88067	protein R52.2 [imp
184	29	70.7	1029	2	S64731	serine/threonine-s

185	29	70.7	1030	2	T16114	hypothetical prote
186	29	70.7	1099	2	H83210	probable phospholi
187	29	70.7	1100	2	T17270	hypothetical prote
188	29	70.7	1216	2	A55620	apical endosomal p
189	29	70.7	1269	2	S35366	furin (EC 3.4.21.7
190	29	70.7	1296	2	T13936	collar protein iso
191	29	70.7	1313	2	G82887	hypothetical prote
192	29	70.7	1401	2	S77657	cyclic peptide syn
193	29	70.7	1451	2	I40325	dermonecrotic toxi
194	29	70.7	1616	2	G64242	cytadherence-acces
195	29	70.7	2073	2	T39207	fatty acid synthas
196	29	70.7	2073	2	T43311	fatty-acyl-CoA syn
197	29	70.7	2076	2	S15999	fatty-acyl-CoA syn
198	29	70.7	2348	2	AD1841	hypothetical prote
199	29	70.7	2411	2	A46299	tyrosine kinase su
200	28	68.3	88	2	AG1970	hypothetical prote
201	28	68.3	108	2	AD0553	hypothetical prote
202	28	68.3	109	2	S50356	sugar transport pr
203	28	68.3	110	2	I39999	hypothetical prote
204	28	68.3	121	2	E75598	hypothetical prote
205	28	68.3	122	2	PQ0791	H ⁺ -transporting tw
206	28	68.3	122	2	PQ0792	H ⁺ -transporting tw
207	28	68.3	132	2	S49160	hypothetical prote
208	28	68.3	136	2	T02322	hypothetical prote
209	28	68.3	136	2	B90199	hypothetical prote
210	28	68.3	146	2	AI2376	hypothetical prote
211	28	68.3	147	2	E82998	conserved hypothet
212	28	68.3	148	2	S35193	oxidase lip19 - ri
213	28	68.3	159	2	C70607	hypothetical prote
214	28	68.3	161	2	G86007	hypothetical prote
215	28	68.3	161	2	F91161	hypothetical prote
216	28	68.3	170	2	AF3312	hypothetical prote
217	28	68.3	179	2	S74894	hypothetical prote
218	28	68.3	194	2	A70695	hypothetical prote
219	28	68.3	194	2	AB1033	hypothetical prote
220	28	68.3	208	2	H82636	hypothetical prote
221	28	68.3	209	2	AI3455	transcription regu
222	28	68.3	211	2	G83718	DNA-binding protei
223	28	68.3	224	2	D75003	hypothetical prote
224	28	68.3	236	1	A32121	snake venom factor
225	28	68.3	236	1	B32121	snake venom factor
226	28	68.3	255	2	S22534	seed protein B32E
227	28	68.3	258	2	AE1819	hypothetical prote
228	28	68.3	261	2	S76737	hypothetical prote
229	28	68.3	264	2	C84195	endonuclease V [im
230	28	68.3	265	2	T52313	photosystem II pro
231	28	68.3	286	2	T46673	probable methylase
232	28	68.3	290	2	AG0204	protein-glutamate
233	28	68.3	297	2	E69152	formylmethanofuran
234	28	68.3	297	2	F69145	hypothetical prote
235	28	68.3	315	2	AD1324	transcription repr
236	28	68.3	315	2	AF1695	transcription repr
237	28	68.3	317	2	AI0686	hypothetical prote
238	28	68.3	342	2	T29989	hypothetical prote
239	28	68.3	358	2	T25790	hypothetical prote
240	28	68.3	368	2	A45610	fructose-bisphosph
241	28	68.3	368	2	T40115	uv excision repair

242	28	68.3	374	2	A42270	alpha (1,3) fucosy
243	28	68.3	389	2	G70769	probable fadA4 pro
244	28	68.3	394	2	E84278	chorismate synthas
245	28	68.3	395	2	T51774	acetyl-CoA C-acety
246	28	68.3	395	2	B81358	transmembrane tran
247	28	68.3	401	2	AI3115	beta-ketoadipyl Co
248	28	68.3	410	2	T13255	hypothetical prote
249	28	68.3	418	2	S44646	hypothetical prote
250	28	68.3	419	2	D98171	beta-ketoadipyl-Co
251	28	68.3	424	2	T29158	hypothetical prote
252	28	68.3	427	1	S06750	basic 7S globulin
253	28	68.3	428	2	AG0219	flagellar hook pro
254	28	68.3	434	1	S61999	hypothetical prote
255	28	68.3	438	2	A64147	hypothetical prote
256	28	68.3	441	2	B86252	hypothetical prote
257	28	68.3	444	1	S75761	cytochrome P450 -
258	28	68.3	447	2	S25817	hypothetical prote
259	28	68.3	457	2	I64184	UDP-N-acetylmuramo
260	28	68.3	465	2	C81427	H+-transporting tw
261	28	68.3	467	1	PWBSBF	H+-transporting tw
262	28	68.3	467	2	F82036	ATP synthase F1, b
263	28	68.3	467	2	S06082	H+-transporting tw
264	28	68.3	467	2	B65020	hypothetical prote
265	28	68.3	467	2	A91043	hypothetical prote
266	28	68.3	467	2	D85887	hypothetical prote
267	28	68.3	469	2	S17726	H+-transporting tw
268	28	68.3	469	2	G72264	glutamate-tRNA lig
269	28	68.3	471	2	A26926	H+-transporting tw
270	28	68.3	471	2	S57449	fusca protein homo
271	28	68.3	473	2	A25504	H+-transporting tw
272	28	68.3	473	2	I40368	H+-transporting tw
273	28	68.3	475	2	S73180	H+-transporting tw
274	28	68.3	476	1	JC2318	angiotensin precur
275	28	68.3	477	2	AH0748	probable exported
276	28	68.3	482	2	AG2435	ATP synthase beta
277	28	68.3	482	2	S36972	H+-transporting tw
278	28	68.3	483	1	PWYBB	H+-transporting tw
279	28	68.3	483	2	AD3425	xylulokinase (EC 2
280	28	68.3	483	2	T47422	cellulase-like pro
281	28	68.3	484	1	PWYCB	H+-transporting tw
282	28	68.3	489	2	A26850	H+-transporting tw
283	28	68.3	494	2	T45480	catalase (EC 1.11.
284	28	68.3	498	1	PWNTB	H+-transporting tw
285	28	68.3	498	1	PWNTB9	H+-transporting tw
286	28	68.3	498	1	PWNTBB	H+-transporting tw
287	28	68.3	498	1	PWNTBC	H+-transporting tw
288	28	68.3	498	1	PWNTBZ	H+-transporting tw
289	28	68.3	500	2	G01646	fusca protein homo
290	28	68.3	501	2	H96778	hypothetical prote
291	28	68.3	503	2	E87101	probable membrane
292	28	68.3	503	2	D70930	hypothetical prote
293	28	68.3	505	1	S71413	betaine-aldehyde d
294	28	68.3	506	2	C42725	amidase (EC 3.5.1.
295	28	68.3	509	2	AI3300	sugar transport AT
296	28	68.3	516	2	C82946	hypothetical prote
297	28	68.3	523	2	C69001	conserved hypothet
298	28	68.3	534	2	E97065	sugar kinase, prob

299	28	68.3	556	2	G86319	F25I16.5 protein -
300	28	68.3	583	2	A70723	probable acyl-coAs
301	28	68.3	604	2	E96762	hypothetical prote
302	28	68.3	624	2	T48587	peptide transporte
303	28	68.3	645	2	S20138	probable protein k
304	28	68.3	648	2	T37581	probable serine-th
305	28	68.3	674	2	T28274	ORF MSV113 probabl
306	28	68.3	681	2	F95885	probable iron ABC
307	28	68.3	684	2	T33785	hypothetical prote
308	28	68.3	690	2	S62728	transposase - phag
309	28	68.3	706	2	G71004	hypothetical prote
310	28	68.3	712	2	T33028	hypothetical prote
311	28	68.3	737	2	A87626	catalase/peroxidas
312	28	68.3	748	2	C82529	conserved hypothet
313	28	68.3	770	1	A44337	kinesin-related pr
314	28	68.3	779	2	T20654	hypothetical prote
315	28	68.3	784	2	T22939	hypothetical prote
316	28	68.3	788	1	F71908	ribonucleoside-dip
317	28	68.3	788	1	H64604	ribonucleoside-dip
318	28	68.3	790	2	S25366	DNA repair protein
319	28	68.3	798	2	H81040	penicillin-binding
320	28	68.3	815	2	T35970	probable efflux pr
321	28	68.3	843	2	H72204	pullulanase - Ther
322	28	68.3	862	2	E84507	hypothetical prote
323	28	68.3	897	2	A39405	beta-galactosidase
324	28	68.3	924	2	AD2154	hypothetical prote
325	28	68.3	940	2	D87006	probable preprotei
326	28	68.3	972	1	GNXSIV	genome polyprotein
327	28	68.3	972	2	T09624	genome polyprotein
328	28	68.3	1070	2	T25836	hypothetical prote
329	28	68.3	1123	2	A44766	defective chorion-
330	28	68.3	1131	2	T15617	hypothetical prote
331	28	68.3	1180	2	T20773	hypothetical prote
332	28	68.3	1183	2	T39233	probable Inositol
333	28	68.3	1187	1	JC4155	protein-tyrosine-p
334	28	68.3	1223	2	T17345	hypothetical prote
335	28	68.3	1379	2	T37752	hypothetical serin
336	28	68.3	1459	2	AI2488	hypothetical prote
337	28	68.3	1606	2	T49219	translation initia
338	28	68.3	1973	2	G89608	protein B0272.5 [i
339	28	68.3	1973	2	T18686	hypothetical prote
340	28	68.3	2305	2	B89608	protein C23F12.1 [
341	28	68.3	2305	2	T15571	hypothetical prote
342	28	68.3	3300	2	D70575	probable PPE prote
343	28	68.3	4549	2	T20771	hypothetical prote
344	28	68.3	4667	2	T20774	hypothetical prote
345	28	68.3	8563	2	T30226	polyketide synthas
346	27	65.9	67	2	A25188	H+-transporting tw
347	27	65.9	67	2	T11406	H+-transporting tw
348	27	65.9	67	2	T11367	H+-transporting tw
349	27	65.9	67	2	T11861	H+-transporting tw
350	27	65.9	67	2	T11251	H+-transporting tw
351	27	65.9	67	2	T11484	H+-transporting tw
352	27	65.9	71	2	S45608	light-harvesting p
353	27	65.9	71	2	D95402	hypothetical prote
354	27	65.9	79	2	C95152	IS66 family elemen
355	27	65.9	79	2	H95167	IS66 family elemen

356	27	65.9	79	2	B98034	degenerate transpo
357	27	65.9	90	2	G84657	hypothetical prote
358	27	65.9	114	2	S46983	indole-3-pyruvate
359	27	65.9	120	2	D72591	hypothetical prote
360	27	65.9	133	2	AB2421	hypothetical prote
361	27	65.9	134	2	D72634	hypothetical prote
362	27	65.9	150	2	E72587	hypothetical prote
363	27	65.9	151	1	R5NT28	ribosomal protein
364	27	65.9	152	2	T15170	hypothetical prote
365	27	65.9	152	2	T28759	hypothetical prote
366	27	65.9	154	2	JQ2228	trans-activating p
367	27	65.9	154	2	S67503	gene X protein - h
368	27	65.9	156	2	B84227	hypothetical prote
369	27	65.9	157	2	G84292	hypothetical prote
370	27	65.9	159	2	S53582	TATA-binding prote
371	27	65.9	163	2	S62536	hypothetical prote
372	27	65.9	168	2	A45943	vitelline membrane
373	27	65.9	173	2	AE1924	hypothetical prote
374	27	65.9	174	2	JV0046	hypothetical 18K p
375	27	65.9	177	2	G82057	ribosomal protein
376	27	65.9	177	2	B64094	ribosomal protein
377	27	65.9	177	2	D71311	hypothetical prote
378	27	65.9	178	2	T44398	ribosomal protein
379	27	65.9	179	2	AG1070	primosomal protein
380	27	65.9	181	2	D85636	hypothetical prote
381	27	65.9	198	1	B64842	trp repressor-bind
382	27	65.9	201	2	S05436	dnaK-type molecula
383	27	65.9	201	2	F86250	hypothetical prote
384	27	65.9	203	2	T02137	hypothetical prote
385	27	65.9	207	2	AI1897	anaerobic ribonucl
386	27	65.9	212	2	H82389	glutaredoxin-relat
387	27	65.9	213	2	T23865	hypothetical prote
388	27	65.9	218	2	AB0254	probable fumarylac
389	27	65.9	219	2	S47082	dnaK-type molecula
390	27	65.9	222	2	T16643	hypothetical prote
391	27	65.9	232	1	A54361	venombin A (EC 3.4
392	27	65.9	233	2	AB0273	probable membrane
393	27	65.9	235	2	A97996	degenerate transpo
394	27	65.9	237	2	T16265	hypothetical prote
395	27	65.9	238	2	AC2568	hypothetical prote
396	27	65.9	238	2	T40820	proline-rich prote
397	27	65.9	250	1	MNVUPT	nonstructural prot
398	27	65.9	251	2	A44844	Al3 antigen - Tryp
399	27	65.9	256	2	A55652	Oct-binding factor
400	27	65.9	256	2	S63588	transcription coac
401	27	65.9	258	2	B82287	conserved hypothet
402	27	65.9	261	2	E70957	probable lprF prot
403	27	65.9	266	2	AF1617	hypothetical prote
404	27	65.9	266	2	AH1254	hypothetical prote
405	27	65.9	268	2	S71830	transcription coac
406	27	65.9	287	2	T01192	hypothetical prote
407	27	65.9	288	2	T10477	sec13 protein - ye
408	27	65.9	289	2	F87110	probable ignal pep
409	27	65.9	296	2	F81155	conserved hypothet
410	27	65.9	305	2	AC2730	conserved hypothet
411	27	65.9	305	2	D97511	probable integral
412	27	65.9	306	2	A56344	copper homeostasis

413	27	65.9	313	2	T15160	hypothetical prote
414	27	65.9	315	2	A90895	hypothetical prote
415	27	65.9	315	2	H85722	hypothetical prote
416	27	65.9	315	2	E64906	probable membrane
417	27	65.9	324	2	E84972	hypothetical prote
418	27	65.9	326	2	A45452	transcription fact
419	27	65.9	331	2	T28023	hypothetical prote
420	27	65.9	333	2	S46984	indole-3-pyruvate
421	27	65.9	333	2	H85551	hypothetical prote
422	27	65.9	333	2	E90701	hypothetical prote
423	27	65.9	333	2	F64783	hypothetical prote
424	27	65.9	333	2	AH2038	hypothetical prote
425	27	65.9	334	2	S65577	replication protei
426	27	65.9	335	2	G64385	hypothetical prote
427	27	65.9	338	2	E83278	probable magnesium
428	27	65.9	342	1	S64322	probable membrane
429	27	65.9	343	1	SZBS2D	stage II sporulati
430	27	65.9	348	2	AF0193	dihydrooorotase (EC
431	27	65.9	356	2	A96826	T8K14.10 [imported
432	27	65.9	357	2	B81965	hemoglobin-haptogl
433	27	65.9	358	2	H75264	hypothetical prote
434	27	65.9	358	2	H72666	hypothetical prote
435	27	65.9	358	2	AE2836	lytic murein trans
436	27	65.9	358	2	H97613	hypothetical prote
437	27	65.9	358	2	T23802	hypothetical prote
438	27	65.9	359	2	T21705	hypothetical prote
439	27	65.9	360	2	G82551	phage-related prot
440	27	65.9	360	2	A82770	phage-related tail
441	27	65.9	361	2	D83026	conserved hypothet
442	27	65.9	362	2	T24046	hypothetical prote
443	27	65.9	363	2	F65070	hypothetical prote
444	27	65.9	363	2	H81104	GTP cyclohydrolase
445	27	65.9	363	2	C81912	probable bifunctio
446	27	65.9	364	1	WFPGA	inhibin alpha chai
447	27	65.9	368	2	E84963	gcpE protein [impo
448	27	65.9	369	2	AG1950	hypothetical prote
449	27	65.9	371	1	A43830	alanine dehydrogen
450	27	65.9	372	2	S72711	masC protein - Myc
451	27	65.9	373	2	T27414	hypothetical prote
452	27	65.9	377	2	AE0845	probable rubredoxi
453	27	65.9	377	2	A35795	carbonate dehydrat
454	27	65.9	380	2	S77053	magnesium/cobalt t
455	27	65.9	380	2	S14188	carbonate dehydrat
456	27	65.9	381	2	T13666	NADH2 dehydrogenas
457	27	65.9	383	2	G95387	probable transcrip
458	27	65.9	385	2	AF0548	penicillin-binding
459	27	65.9	389	2	AH3003	penicillin-binding
460	27	65.9	390	1	B49070	ecdysone-inducible
461	27	65.9	390	2	E88925	protein T22H9.4 [i
462	27	65.9	391	2	S48967	ethanolaminephosph
463	27	65.9	394	2	E83903	thiolase (acetyl-C
464	27	65.9	394	2	C36942	hypothetical prote
465	27	65.9	394	2	T02190	hypothetical prote
466	27	65.9	396	1	S17929	transcription init
467	27	65.9	396	2	C85942	probable carbamoyl
468	27	65.9	396	2	G91096	probable carbamoyl
469	27	65.9	396	2	S41224	hnRNP protein - Af

470	27	65.9	398	2	T40074	hypothetical zf-C3
471	27	65.9	398	2	A99280	penicillin-binding
472	27	65.9	402	2	S61413	DNA-binding protei
473	27	65.9	402	2	T52522	hypothetical prote
474	27	65.9	405	2	G84200	cytochrome P450 [i
475	27	65.9	405	2	A96917	probable permease
476	27	65.9	408	2	F86444	hypothetical prote
477	27	65.9	410	1	DEBYPX	pyruvate dehydroge
478	27	65.9	410	2	E72397	hypothetical prote
479	27	65.9	413	2	AH2743	conserved hypothet
480	27	65.9	414	2	B56711	casein kinase I (E
481	27	65.9	415	2	AD0568	conserved hypothet
482	27	65.9	416	2	G97524	hypothetical prote
483	27	65.9	416	2	S16658	mobilization prote
484	27	65.9	424	2	D69399	3-ketoacyl-CoA thi
485	27	65.9	424	2	F69723	trigger factor tig
486	27	65.9	431	2	T20263	hypothetical prote
487	27	65.9	434	2	AH1993	hypothetical prote
488	27	65.9	439	2	AC1182	probable sugar ABC
489	27	65.9	440	2	AD1539	probable sugar ABC
490	27	65.9	441	2	C84634	hypothetical prote
491	27	65.9	442	2	H69181	hypothetical prote
492	27	65.9	447	2	E96008	probable glycosylt
493	27	65.9	448	2	AD0703	probable transport
494	27	65.9	448	2	C56711	casein kinase I (E
495	27	65.9	450	1	WABPT5	gene D10 protein -
496	27	65.9	450	2	A44751	carotenoid-binding
497	27	65.9	454	2	A54693	CACCC box-binding
498	27	65.9	457	2	A25351	ubiquinol-cytochro
499	27	65.9	458	2	D88950	protein R09B5.1 [i
500	27	65.9	463	2	S41495	dC stretch-binding
501	27	65.9	464	2	F83365	lipoamide dehydrog
502	27	65.9	464	2	A54143	kappa-B motif-bind
503	27	65.9	464	2	S43363	transformation upr
504	27	65.9	469	2	S41496	rad22 protein - fi
505	27	65.9	478	2	E90495	aldehyde dehydroge
506	27	65.9	478	2	S56904	hypothetical prote
507	27	65.9	479	1	S15031	paired box transcr
508	27	65.9	479	2	G64710	hypothetical prote
509	27	65.9	479	2	D71809	hypothetical prote
510	27	65.9	481	2	C96936	lysine decarboxyla
511	27	65.9	486	2	S36190	transmembrane prot
512	27	65.9	488	1	I39769	aldehyde dehydroge
513	27	65.9	488	2	G69752	aldehyde dehydroge
514	27	65.9	489	2	T27468	hypothetical prote
515	27	65.9	490	2	AF0156	probable D-mannona
516	27	65.9	491	2	C75078	hypothetical prote
517	27	65.9	491	2	B75554	hypothetical prote
518	27	65.9	495	2	T26300	hypothetical prote
519	27	65.9	496	2	A49930	carB protein homol
520	27	65.9	498	2	AD2277	aldehyde dehydroge
521	27	65.9	500	2	F83418	sodium/proton anti
522	27	65.9	501	2	T19590	hypothetical prote
523	27	65.9	503	2	G84234	aldehyde dehydroge
524	27	65.9	503	2	D75437	DNA repair protein
525	27	65.9	505	2	T03394	probable betaine-a
526	27	65.9	517	2	D88987	protein C50H11.1 [

527	27	65.9	520	2	T21666	hypothetical prote
528	27	65.9	522	2	B64067	Na ⁺ /H ⁺ -exchanging
529	27	65.9	529	2	AB2069	hypothetical prote
530	27	65.9	531	2	T49936	hypothetical prote
531	27	65.9	533	2	T39025	hypothetical prote
532	27	65.9	547	2	H90668	probable receptor
533	27	65.9	547	2	C85519	probable receptor
534	27	65.9	547	2	B64755	yagW protein - Esc
535	27	65.9	550	1	VGBEG5	glycoprotein E pre
536	27	65.9	552	1	VGBEKD	glycoprotein E pre
537	27	65.9	552	2	T44954	flagella-related p
538	27	65.9	554	2	S22495	pollen-specific pr
539	27	65.9	558	2	B87098	conserved hypothet
540	27	65.9	559	2	A57474	extracellular matr
541	27	65.9	560	2	AD2389	serine/threonine k
542	27	65.9	568	2	S15008	gene disco protein
543	27	65.9	569	2	H87926	protein C17D12.7 [
544	27	65.9	570	2	T04836	probable serine/th
545	27	65.9	573	2	T21653	hypothetical prote
546	27	65.9	575	2	C90143	hypothetical prote
547	27	65.9	575	2	T29972	hypothetical prote
548	27	65.9	578	2	A70877	probable acyl-coAs
549	27	65.9	578	2	D69165	hypothetical prote
550	27	65.9	579	2	B86926	acyl-CoA synthetas
551	27	65.9	579	2	D87063	probable acyl-CoA
552	27	65.9	580	2	B70668	probable Acyl-CoA
553	27	65.9	583	2	AE3308	2-isopropylmalate
554	27	65.9	588	2	JC5797	F0F1-ATPase (EC 3.
555	27	65.9	594	2	T06467	phosphoinositide-s
556	27	65.9	600	2	D83286	hypothetical prote
557	27	65.9	603	2	T46236	hypothetical prote
558	27	65.9	614	2	S42526	finger protein unk
559	27	65.9	615	2	C75278	DNA polymerase III
560	27	65.9	616	2	C75588	conserved hypothet
561	27	65.9	621	2	S72493	laccase (EC 1.10.3
562	27	65.9	621	2	T48492	hypothetical prote
563	27	65.9	627	2	AE1818	N-acetylmuramoyl-L
564	27	65.9	631	2	D96683	hypothetical prote
565	27	65.9	641	2	G85043	hypothetical prote
566	27	65.9	642	2	G72265	hypothetical prote
567	27	65.9	643	2	T19199	hypothetical prote
568	27	65.9	651	2	F95045	transcription regu
569	27	65.9	651	2	E97916	conserved hypothet
570	27	65.9	651	2	S24609	cytoskeletal prote
571	27	65.9	668	2	C24785	hypothetical prote
572	27	65.9	670	2	T02019	callus-associated
573	27	65.9	687	2	T47403	amine oxidase-like
574	27	65.9	688	2	S73930	translation elonga
575	27	65.9	693	2	D90441	ABC transporter, p
576	27	65.9	694	2	AI2492	hypothetical prote
577	27	65.9	698	2	AC0016	4-alpha-glucanotra
578	27	65.9	700	2	B82788	metallopeptidase X
579	27	65.9	706	2	E30411	synapsin Ia - bovi
580	27	65.9	706	2	D84466	hypothetical prote
581	27	65.9	709	2	T00664	hypothetical prote
582	27	65.9	715	2	G86239	protein F20B24.6 [
583	27	65.9	718	2	T20673	hypothetical prote

584	27	65.9	719	2	S63629	homeotic protein A
585	27	65.9	732	2	A43315	ETS domain protein
586	27	65.9	739	2	A55314	glycine-tRNA ligas
587	27	65.9	741	2	T00206	epidermis-specific
588	27	65.9	756	2	AD1422	beta-glucosidase h
589	27	65.9	761	2	A46193	88K E-26-specific
590	27	65.9	762	2	S56141	HAK1 protein - yea
591	27	65.9	768	1	BVBY23	protein transport
592	27	65.9	775	2	S63626	homeotic protein A
593	27	65.9	784	2	JH0101	apolipoprotein B-1
594	27	65.9	792	2	B82752	penicillin binding
595	27	65.9	795	2	T49835	hypothetical prote
596	27	65.9	796	2	T43782	hypothetical prote
597	27	65.9	809	2	F81312	leucine-tRNA ligas
598	27	65.9	819	1	S40400	protein kinase SWE
599	27	65.9	829	2	I46536	Ksp-cadherin - rab
600	27	65.9	837	2	E70835	hypothetical glyci
601	27	65.9	847	2	S75975	hypothetical prote
602	27	65.9	852	1	VCLJBR	env polyprotein -
603	27	65.9	856	2	B81399	probable periplasm
604	27	65.9	864	2	A49070	ecdysone-inducible
605	27	65.9	876	2	T07101	lipoxxygenase (EC 1
606	27	65.9	877	1	IJBOCN	N-cadherin precurs
607	27	65.9	884	2	AE3166	ATP-dependent DNA
608	27	65.9	891	2	G41662	130K surface exclu
609	27	65.9	906	1	IJHUCN	cadherin 2 precurs
610	27	65.9	906	1	IJMSCN	N-cadherin precurs
611	27	65.9	911	2	A56465	transcription fact
612	27	65.9	927	2	T24031	hypothetical prote
613	27	65.9	937	2	A35553	beta-adaptin - hum
614	27	65.9	937	2	C35553	beta-adaptin - rat
615	27	65.9	952	2	A99823	probable tail leng
616	27	65.9	968	2	T00353	hypothetical prote
617	27	65.9	969	2	A75634	McrB-related prote
618	27	65.9	969	2	B85843	probable tail comp
619	27	65.9	995	2	T22942	hypothetical prote
620	27	65.9	1007	2	H81670	conserved hypothet
621	27	65.9	1026	2	C90854	probable tail leng
622	27	65.9	1026	2	G90876	probable tail leng
623	27	65.9	1026	2	F85692	probable tail comp
624	27	65.9	1044	2	T37568	hypothetical prote
625	27	65.9	1052	2	T00067	hypothetical prote
626	27	65.9	1054	2	A61221	probable calcium t
627	27	65.9	1058	2	S65460	apolipoprotein B -
628	27	65.9	1072	2	S76888	hypothetical prote
629	27	65.9	1080	2	H90908	probable tail leng
630	27	65.9	1120	2	H88449	protein F54D8.1 [i
631	27	65.9	1192	2	T13424	hypothetical prote
632	27	65.9	1197	2	I39613	pyruvate (flavodox
633	27	65.9	1199	2	AD2156	pyruvate-flavodoxi
634	27	65.9	1208	2	T23222	hypothetical prote
635	27	65.9	1217	2	T00270	hypothetical prote
636	27	65.9	1236	2	E70977	hypothetical prote
637	27	65.9	1277	2	T32731	PAR interacting pr
638	27	65.9	1337	2	T38949	hypothetical prote
639	27	65.9	1356	2	S51389	ROM2 protein - yea
640	27	65.9	1383	2	T13052	guanine nucleotide

641	27	65.9	1396	2	G70598	hypothetical prote
642	27	65.9	1516	2	T01055	hypothetical prote
643	27	65.9	1582	2	AC1153	adhesin homolog lm
644	27	65.9	1607	2	T13250	hypothetical prote
645	27	65.9	1626	2	T29093	hypothetical prote
646	27	65.9	1647	2	T41267	hypothetical prote
647	27	65.9	1668	2	T13748	sex comb protein -
648	27	65.9	1778	2	JT0382	apolipoprotein B -
649	27	65.9	1926	2	JC4842	DNA-binding nuclea
650	27	65.9	2137	2	T05244	hypothetical prote
651	27	65.9	2180	2	A47651	zinc-finger protei
652	27	65.9	2325	2	A61208	chondroitin sulfat
653	27	65.9	2338	2	T25810	hypothetical prote
654	27	65.9	2440	2	S39162	transcription coac
655	27	65.9	2629	2	I46569	apolipoprotein B -
656	27	65.9	3158	2	T17483	peptide synthetase
657	27	65.9	3229	2	S27852	probable cell-surf
658	27	65.9	3655	2	T38084	TRAP-like protein
659	27	65.9	3744	2	S46715	hypothetical prote
660	27	65.9	4273	2	C69679	polyketide synthas
661	27	65.9	4563	1	LPHUB	apolipoprotein B-1
662	26.5	64.6	165	2	A71105	hypothetical prote
663	26.5	64.6	270	2	AG0916	probable hydrolase
664	26.5	64.6	274	2	D81013	DNA ligase NMB2048
665	26.5	64.6	274	2	B81955	probable secreted
666	26.5	64.6	293	2	F86070	probable enzyme Z5
667	26.5	64.6	293	2	H91223	probable enzyme [i
668	26.5	64.6	349	2	T49791	hypothetical prote
669	26	63.4	24	2	B53524	ubiquinol-cytochro
670	26	63.4	42	1	CBKT5F	cytochrome b559 co
671	26	63.4	44	2	S73311	cytochrome b559 be
672	26	63.4	65	1	NTSR1B	neurotoxin I - sco
673	26	63.4	66	1	NTSR9E	neurotoxin M9 - le
674	26	63.4	69	2	B46238	hypothetical prote
675	26	63.4	76	2	E97763	protein transport
676	26	63.4	77	2	AF0074	probable membrane
677	26	63.4	89	2	T33460	hypothetical prote
678	26	63.4	93	2	JQ1761	hypothetical 9.9K
679	26	63.4	95	2	B84181	hypothetical prote
680	26	63.4	100	2	A71018	hypothetical prote
681	26	63.4	107	2	S75401	hypothetical prote
682	26	63.4	108	2	AG0699	probable pathogeni
683	26	63.4	110	2	G72597	hypothetical prote
684	26	63.4	119	2	T36326	probable dihydrone
685	26	63.4	126	2	A87218	hypothetical prote
686	26	63.4	132	1	QQCVL3	AL3 protein - toma
687	26	63.4	134	2	T32913	hypothetical prote
688	26	63.4	134	2	C87723	protein C54G6.4 [i
689	26	63.4	137	2	T22475	hypothetical prote
690	26	63.4	138	2	I39641	toxin I - Actinoba
691	26	63.4	138	2	B46348	gene A2-A3 protein
692	26	63.4	138	2	A71333	hypothetical prote
693	26	63.4	139	2	E85845	unknown protein en
694	26	63.4	142	2	S63373	probable membrane
695	26	63.4	148	2	C90780	hypothetical prote
696	26	63.4	148	2	B85641	hypothetical prote
697	26	63.4	151	2	AE1938	hypothetical prote

698	26	63.4	154	2	AF3354	translation initia
699	26	63.4	169	2	F87713	conserved hypothet
700	26	63.4	171	2	T46342	hypothetical prote
701	26	63.4	177	2	G87254	inorganic pyrophos
702	26	63.4	179	1	RMECI	replication termin
703	26	63.4	179	2	E86135	DNA biosynthesis,
704	26	63.4	179	2	B91294	primosomal protein
705	26	63.4	179	2	AI2060	hypothetical prote
706	26	63.4	180	2	T07702	hypothetical prote
707	26	63.4	182	2	H69026	ribosomal protein
708	26	63.4	183	2	E75281	transcription elon
709	26	63.4	184	2	D70257	outer membrane pro
710	26	63.4	186	2	H75004	hypothetical prote
711	26	63.4	188	2	A71186	probable ribosomal
712	26	63.4	191	2	S54295	GTP-binding protei
713	26	63.4	192	1	B34386	GTP-binding protei
714	26	63.4	192	2	S51718	GTP-binding protei
715	26	63.4	192	2	A60194	GTP-binding protei
716	26	63.4	193	2	B71170	hypothetical prote
717	26	63.4	193	2	T05475	hypothetical prote
718	26	63.4	196	2	T50018	MADS box protein F
719	26	63.4	197	2	S57948	HMG1/Y protein - g
720	26	63.4	198	2	D82253	dedD protein VC100
721	26	63.4	200	2	A40797	ubiquitin-conjugat
722	26	63.4	201	2	S74907	hypothetical prote
723	26	63.4	202	2	T46523	probable cyclase-d
724	26	63.4	204	2	T05575	hypothetical prote
725	26	63.4	204	2	S75304	serine esterase -
726	26	63.4	204	2	A83357	hypothetical prote
727	26	63.4	209	2	AH0219	flagellar basal-bo
728	26	63.4	212	2	H87060	probable secreted
729	26	63.4	214	2	A87276	hypothetical prote
730	26	63.4	214	2	AF2727	exoD protein [impo
731	26	63.4	215	2	S48445	hypothetical prote
732	26	63.4	216	2	T15317	hypothetical prote
733	26	63.4	218	2	T47706	hypothetical prote
734	26	63.4	221	2	S58685	hypothetical prote
735	26	63.4	224	2	T10660	photosystem II pro
736	26	63.4	224	2	E95223	hypothetical prote
737	26	63.4	224	2	H98087	hypothetical prote
738	26	63.4	225	2	S45356	probable serine pr
739	26	63.4	225	2	D64506	hypothetical prote
740	26	63.4	225	2	C71159	hypothetical prote
741	26	63.4	228	2	A97509	exod protein [impo
742	26	63.4	229	2	S57654	glutenin low molec
743	26	63.4	229	2	S46696	hypothetical prote
744	26	63.4	231	2	G70505	hypothetical prote
745	26	63.4	231	2	T48215	translation initia
746	26	63.4	232	2	S72930	hypothetical prote
747	26	63.4	233	2	AG0779	FAA-hydrolase-fami
748	26	63.4	233	2	E91007	probable isomerase
749	26	63.4	233	2	G85851	probable isomerase
750	26	63.4	235	2	F70386	flagellar motor pr
751	26	63.4	235	2	C81991	hypothetical prote
752	26	63.4	235	2	G81219	hypothetical prote
753	26	63.4	238	2	G83126	probable short-cha
754	26	63.4	238	2	B64509	hypothetical prote

755	26	63.4	239	2	D96587	hypothetical prote
756	26	63.4	240	2	A39480	exopolysaccharide
757	26	63.4	240	2	S31573	hypothetical prote
758	26	63.4	242	2	S25663	T-cell surface gly
759	26	63.4	243	1	JQ0021	ubiquinol-cytochro
760	26	63.4	243	2	S07976	B1-hordein (clone
761	26	63.4	244	2	S07398	gamma-gliadin B pr
762	26	63.4	246	1	S49770	hypothetical prote
763	26	63.4	246	2	S72718	probable invasion
764	26	63.4	252	2	AC2861	conserved hypothet
765	26	63.4	255	1	ASLJSZ	nef protein - huma
766	26	63.4	255	2	AD1840	hypothetical prote
767	26	63.4	256	1	ASLJH2	nef protein - huma
768	26	63.4	256	2	T45895	hypothetical prote
769	26	63.4	260	2	AF0081	conserved hypothet
770	26	63.4	261	2	S40162	cathepsin G (EC 3.
771	26	63.4	261	2	S57655	glutenin low molec
772	26	63.4	266	2	D75483	hypothetical prote
773	26	63.4	272	2	S28013	outC protein - Erw
774	26	63.4	273	2	S40003	trypsin-related pr
775	26	63.4	273	2	AI1989	hypothetical prote
776	26	63.4	275	2	S40007	trypsin (EC 3.4.21
777	26	63.4	276	2	S57656	glutenin low molec
778	26	63.4	276	2	C75508	hypothetical prote
779	26	63.4	276	2	B97638	hypothetical prote
780	26	63.4	277	2	G75505	hypothetical prote
781	26	63.4	277	2	T37629	hypothetical prote
782	26	63.4	278	2	T35379	hypothetical prote
783	26	63.4	279	2	T16736	hypothetical prote
784	26	63.4	279	2	D82153	transcription regu
785	26	63.4	283	2	AE0211	conserved hypothet
786	26	63.4	284	2	T18253	probable mitochond
787	26	63.4	286	2	T05910	glutenin low molec
788	26	63.4	288	2	T05954	transcription fact
789	26	63.4	289	2	T22834	hypothetical prote
790	26	63.4	293	2	S07365	hordein B1 - barle
791	26	63.4	294	2	T22639	hypothetical prote
792	26	63.4	295	2	A44984	collagen - nematod
793	26	63.4	295	2	T43463	hypothetical prote
794	26	63.4	297	2	A98294	hypothetical prote
795	26	63.4	297	2	AH2989	permease [imported
796	26	63.4	298	2	T06980	glutenin low molec
797	26	63.4	298	2	S75205	hypothetical prote
798	26	63.4	299	2	T35844	dihydrodipicolinat
799	26	63.4	300	2	T27158	hypothetical prote
800	26	63.4	300	2	G87999	protein Y54E5A.1 [
801	26	63.4	303	2	T06981	low-molecular-weig
802	26	63.4	304	2	T06505	glutenin low molec
803	26	63.4	304	2	I39049	alpha (1,3) fucosy
804	26	63.4	305	2	F84998	diaminopimelate ep
805	26	63.4	305	2	T52287	probable histone d
806	26	63.4	307	2	S04325	glutenin low molec
807	26	63.4	307	2	C96997	ferrichrome-bindin
808	26	63.4	309	2	T46226	hypothetical prote
809	26	63.4	310	2	T22641	hypothetical prote
810	26	63.4	310	2	E84612	homeodomain transc
811	26	63.4	311	1	WNJXL	photosynthetic rea

812	26	63.4	311	2	S47136	homeotic protein A
813	26	63.4	313	2	F71939	hypothetical prote
814	26	63.4	314	2	D87592	dnaJ family protei
815	26	63.4	314	2	G64651	hypothetical prote
816	26	63.4	315	2	AD3127	hypothetical prote
817	26	63.4	315	2	T15165	hypothetical prote
818	26	63.4	316	2	AD2470	hypothetical prote
819	26	63.4	317	2	T39736	hypothetical prote
820	26	63.4	319	2	E98160	hypothetical prote
821	26	63.4	323	2	T06506	glutenin low molec
822	26	63.4	324	2	T35090	probable ABC trans
823	26	63.4	325	2	S57977	CCCH zinc finger p
824	26	63.4	328	2	E81257	probable hemein up
825	26	63.4	330	2	F71146	hypothetical prote
826	26	63.4	331	2	A71128	probable iron (III
827	26	63.4	332	1	WGSMHH	hygromycin B phosp
828	26	63.4	332	2	AC0260	hypothetical phage
829	26	63.4	333	2	JX0343	triacylglycerol li
830	26	63.4	335	2	G86326	protein F18014.7 [
831	26	63.4	337	2	G87487	conserved hypothet
832	26	63.4	338	2	H82275	toxin co-regulated
833	26	63.4	338	2	JN0526	tcpF protein precu
834	26	63.4	341	2	S64618	hypothetical prote
835	26	63.4	342	2	C88579	protein tbx-8 [imp
836	26	63.4	342	2	E75008	hypothetical prote
837	26	63.4	344	1	SZBS2N	stage II sporulati
838	26	63.4	344	2	T33421	hypothetical prote
839	26	63.4	347	2	S00549	developmental cont
840	26	63.4	349	2	S03575	DNA-directed RNA p
841	26	63.4	350	1	D64848	yceA protein - Esc
842	26	63.4	350	2	A99808	hypothetical prote
843	26	63.4	350	2	E85667	hypothetical prote
844	26	63.4	350	2	D75274	hypothetical prote
845	26	63.4	352	2	B85518	hypothetical prote
846	26	63.4	354	1	PNFMGF	peptide-N4- (N-acet
847	26	63.4	355	2	AD0299	conserved hypothet
848	26	63.4	356	2	AC0909	trypsin-like prote
849	26	63.4	357	2	G75552	riboflavin bifunct
850	26	63.4	359	2	A45156	alpha- (1,3)-fucosy
851	26	63.4	360	2	G72235	hypothetical prote
852	26	63.4	362	1	B70382	chorismate mutase/
853	26	63.4	362	2	T35287	probable secreted
854	26	63.4	363	2	T40350	probable polyadeny
855	26	63.4	364	2	I39048	alpha (1,3) fucosy
856	26	63.4	366	2	T47360	hypothetical prote
857	26	63.4	366	2	T26449	hypothetical prote
858	26	63.4	367	2	A70550	probable pdhA prot
859	26	63.4	370	2	A95416	probable enoyl red
860	26	63.4	370	2	AG0359	probable membrane-
861	26	63.4	373	2	B75276	DNA-binding respon
862	26	63.4	376	2	S16386	hypothetical prote
863	26	63.4	377	2	AI0580	rare lipoprotein A
864	26	63.4	378	2	F90667	hypothetical prote
865	26	63.4	378	2	F64300	formate dehydrogen
866	26	63.4	379	2	D91078	probable lipoprote
867	26	63.4	379	2	E85923	lipoprotein [impor
868	26	63.4	379	2	B55522	lipoprotein D prec

869	26	63.4	381	2	T48623	hypothetical prote
870	26	63.4	383	2	D75288	carbohydrate kinas
871	26	63.4	384	1	BVECCX	membrane protein c
872	26	63.4	384	2	AD0049	hypothetical prote
873	26	63.4	386	2	T19354	hypothetical prote
874	26	63.4	389	2	B70400	ferredoxin oxidore
875	26	63.4	389	2	A97577	hypothetical prote
876	26	63.4	389	2	AH2797	conserved hypothet
877	26	63.4	391	2	S74842	phosphoribosylglyc
878	26	63.4	392	2	A84125	acetyl-CoA acetyl
879	26	63.4	393	1	VGBEDZ	glycoprotein D pre
880	26	63.4	393	2	S06256	hypothetical prote
881	26	63.4	394	1	A47627	glycoprotein D pre
882	26	63.4	394	1	VGBE17	glycoprotein D pre
883	26	63.4	394	1	VGBED1	glycoprotein D - h
884	26	63.4	394	2	S29276	acetyl-CoA C-acety
885	26	63.4	395	2	D87572	hypothetical prote
886	26	63.4	396	2	C82769	phage-related cont
887	26	63.4	397	1	VPXR11	inner capsid prote
888	26	63.4	397	1	VPXR6H	inner capsid prote
889	26	63.4	397	1	VPXR6S	inner capsid prote
890	26	63.4	397	1	VPXRGT	inner capsid prote
891	26	63.4	397	1	VPXRS2	inner capsid prote
892	26	63.4	397	2	JQ2020	inner capsid prote
893	26	63.4	397	2	S30582	VP6 protein - huma
894	26	63.4	397	2	T11777	phosphoglycerate t
895	26	63.4	398	2	A36926	aspartyl proteinas
896	26	63.4	398	2	A45280	candidapepsin (EC
897	26	63.4	399	2	T01345	hypothetical prote
898	26	63.4	403	2	AI0604	probable membrane
899	26	63.4	403	2	AB0640	flagellar hook pro
900	26	63.4	403	2	S10365	flagellar hook pro
901	26	63.4	406	2	H72315	conserved hypothet
902	26	63.4	406	2	AF2631	hypothetical prote
903	26	63.4	407	2	H97413	hypothetical prote
904	26	63.4	407	2	T19176	hypothetical prote
905	26	63.4	408	2	T44859	glycosyltransferas
906	26	63.4	410	2	S26669	retinoic acid rece
907	26	63.4	417	2	T04955	hypothetical prote
908	26	63.4	417	2	JE0191	calcium/calmodulin
909	26	63.4	418	2	A53965	bile acid-CoA amin
910	26	63.4	422	2	S37280	cyclin A - mouse
911	26	63.4	422	2	S38501	cyclin A2 - mouse
912	26	63.4	424	2	T33839	hypothetical prote
913	26	63.4	428	2	T39053	hypothetical prote
914	26	63.4	428	2	S45361	LRR47 protein - fr
915	26	63.4	429	2	S19483	probable membrane
916	26	63.4	430	2	T47014	hypothetical prote
917	26	63.4	430	2	AC0237	probable membrane
918	26	63.4	432	2	T33833	hypothetical prote
919	26	63.4	440	2	JC8032	PU.1-binding prote
920	26	63.4	441	2	S33066	malate dehydrogena
921	26	63.4	441	2	G82211	response regulator
922	26	63.4	441	2	T23461	hypothetical prote
923	26	63.4	446	2	A34418	H-2 region II bind
924	26	63.4	447	2	S53309	n-6 fatty acid des
925	26	63.4	448	2	D41727	retinoid X recepto

926	26	63.4	450	2	A86919	probable membrane
927	26	63.4	451	2	A41651	retinoic acid rece
928	26	63.4	452	2	T22948	hypothetical prote
929	26	63.4	454	2	T42680	hypothetical prote
930	26	63.4	455	2	A65062	L-serine ammonia-l
931	26	63.4	455	2	C85931	L-serine dehydrata
932	26	63.4	455	2	A98086	L-serine dehydrata
933	26	63.4	455	2	A87913	protein B0205.10 [
934	26	63.4	455	2	F70564	probable serine pr
935	26	63.4	456	2	A40492	early growth respo
936	26	63.4	457	2	T04226	hypothetical prote
937	26	63.4	464	1	S47454	amidase homolog YM
938	26	63.4	465	2	AC0396	probable amidase [
939	26	63.4	466	1	TWFF	transcription fact
940	26	63.4	469	1	RGKBCP	nitrogen regulatio
941	26	63.4	469	2	T46135	endo-polygalacturo
942	26	63.4	470	2	AD0888	SufI protein [impo
943	26	63.4	470	2	E91116	suppressor of ftsI
944	26	63.4	470	2	E85961	suppressor of ftsI
945	26	63.4	470	2	G65088	sufI protein precu
946	26	63.4	470	2	S02068	RNA-directed RNA p
947	26	63.4	470	2	JN0431	RNA-directed RNA p
948	26	63.4	472	2	S36548	L2 protein - human
949	26	63.4	473	2	S53119	RNA-directed RNA p
950	26	63.4	473	2	A47284	myocyte enhancer-b
951	26	63.4	474	2	E91298	catabolite repress
952	26	63.4	474	2	G86139	hypothetical prote
953	26	63.4	474	2	T00699	hypothetical prote
954	26	63.4	475	2	AC1926	hypothetical prote
955	26	63.4	477	2	A95990	probable dehydroge
956	26	63.4	477	2	AF3469	aldehyde dehydroge
957	26	63.4	478	2	C87351	aldehyde dehydroge
958	26	63.4	478	2	T04519	hypothetical prote
959	26	63.4	479	1	S41015	transcription fact
960	26	63.4	480	2	S34547	H+-transporting tw
961	26	63.4	483	2	A97744	isocitrate dehydro
962	26	63.4	483	2	E71681	isocitrate dehydro
963	26	63.4	486	2	C96699	hypothetical prote
964	26	63.4	487	2	T34858	catalase (EC 1.11.
965	26	63.4	488	2	T14829	H+-transporting tw
966	26	63.4	488	2	G65216	hypothetical 53.4
967	26	63.4	491	2	B69104	conserved hypothet
968	26	63.4	492	1	PWFNBT	H+-transporting tw
969	26	63.4	492	2	S71146	H+-transporting tw
970	26	63.4	492	2	T07492	H+-transporting tw
971	26	63.4	492	2	A59105	hypothetical prote
972	26	63.4	493	1	ACRYB1	nicotinic acetylch
973	26	63.4	494	2	S48769	hypothetical prote
974	26	63.4	495	2	T05388	hypothetical prote
975	26	63.4	498	1	PWBHB	H+-transporting tw
976	26	63.4	498	1	PWRZB	H+-transporting tw
977	26	63.4	498	1	PWSPB	H+-transporting tw
978	26	63.4	498	1	PWWTB	H+-transporting tw
979	26	63.4	498	2	H97214	endoglucanase, fam
980	26	63.4	500	1	JC2231	prostaglandin-I sy
981	26	63.4	501	2	S76581	hypothetical prote
982	26	63.4	503	2	AC3148	exopolysaccharide

983	26	63.4	508	2	S74537	anthranilate synth
984	26	63.4	512	2	S74561	hypothetical prote
985	26	63.4	515	2	AD1048	conserved hypothet
986	26	63.4	515	2	G91271	hypothetical prote
987	26	63.4	515	2	G86112	hypothetical prote
988	26	63.4	515	2	S56392	hypothetical 54.7K
989	26	63.4	515	2	F70904	hypothetical prote
990	26	63.4	517	2	E95920	probable PST type
991	26	63.4	517	2	C89840	conserved hypothet
992	26	63.4	519	2	JC1112	H+-transporting tw
993	26	63.4	520	2	I84718	RXR-betal isoform
994	26	63.4	520	2	H64510	hypothetical prote
995	26	63.4	521	2	T01107	hypothetical prote
996	26	63.4	522	2	S52216	viral proteinase -
997	26	63.4	523	1	O4CKA3	cytochrome P450 52
998	26	63.4	523	2	T36677	probable secretory
999	26	63.4	525	2	S17211	H+-transporting tw
1000	26	63.4	525	2	AF3274	hypothetical prote

ALIGNMENTS

RESULT 1

T12546

hypothetical protein DKFZp586K2120.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12546

R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999

A;Reference number: Z17524

A;Accession: T12546

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1005 <WAM>

A;Cross-references: UNIPROT:Q9H2P0; UNIPARC:UPI000016AC5D; EMBL:AL080163

A;Experimental source: adult uterus; clone DKFZp586K2120

C;Genetics:

A;Note: DKFZp586K2120.1

Query Match 100.0%; Score 41; DB 2; Length 1005;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 257 NAPVSIPQ 264

RESULT 2

B83404

hypothetical protein PA1941 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: B83404

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: B83404

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-631 <STO>

A;Cross-references: UNIPROT:Q9I2G3; UNIPARC:UPI00000C551D; GB:AE004620;

GB:AE004091; NID:g9947929; PIDN:AAG05329.1; GSPDB:GN00131; PASP:PA1941

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA1941

Query Match 87.8%; Score 36; DB 2; Length 631;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
||| ||
Db 263 NAPVSYPQ 270

RESULT 3

D95412

hypothetical protein Sma2233 [imported] - *Sinorhizobium meliloti* (strain 1021) megaplasmid pSymA

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: D95412

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowser, L.; Capela, D.; Galibert, F.; Gouzy, J.; Gurjal, M.; Hong, A.; Huizar, L.; Hyman, R.W.; Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Davis, R.W.; Federspiel, N.A.; Long, S.R.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* pSymA megaplasmid.

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95412

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-299 <KUR>

A;Cross-references: UNIPROT:Q92XP0; UNIPARC:UPI00000CB348; GB:AE006469;

PIDN:AAK65862.1; PID:g14524369; GSPDB:GN00165

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.;

Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMA2233
 A;Genome: plasmid

Query Match 85.4%; Score 35; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
 |||||
 Db 6 APVSIPQ 12

RESULT 4

G69440

conserved hypothetical protein AF1528 - *Archaeoglobus fulgidus*

C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69440

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69440

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-136 <KLE>

A;Cross-references: UNIPROT:O28744; UNIPARC:UPI0000056CC7; GB:AE000997;

GB:AE000782; NID:g2689320; PIDN:AAB89720.1; PID:g2649036; TIGR:AF1528

Query Match 82.9%; Score 34; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 9.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 ||| |:|
 Db 29 NAPFSLPQ 36

RESULT 5

T30248

fragile X mental retardation protein 2 - mouse

N;Alternate names: fmr2 protein

C;Species: Mus musculus (house mouse)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30248

R;Chakrabarti, L.; Bristulf, J.; Foss, G.S.; Davies, K.E.

Hum. Mol. Genet. 7, 441-448, 1998

A;Title: Expression of the murine homologue of FMR2 in mouse brain and during development.

A;Reference number: Z20786; MUID:98133924; PMID:9467002

A;Accession: T30248

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1272 <CHA>

A;Cross-references: UNIPROT:O55112; UNIPARC:UPI0000027ACC; EMBL:AJ001549;

NID:g2832399; PIDN:CAA04821.1; PID:g2832400

A;Experimental source: brain

C;Genetics:

A;Gene: fmr2

A;Note: fmr2 expression in an embryo at 11 days is evident to the roof of the hind brain and the lateral ventricle of the brain

Query Match 82.9%; Score 34; DB 2; Length 1272;

Best Local Similarity 75.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

| ||:|

Db 1191 NGPVTIPQ 1198

RESULT 6

AI0632

trp repressor binding protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C;Accession: AI0632

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebahia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AI0632

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-198 <PAR>
A;Cross-references: UNIPARC:UPI0000059FE4; GB:AL513382; PIDN:CAD08244.1;
PID:g16502291; GSPDB:GN00176
C;Genetics:
A;Gene: STY1155
C;Superfamily: flavodoxin; flavodoxin homology
C;Keywords: flavoprotein

Query Match 80.5%; Score 33; DB 2; Length 198;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||: ||
Db 57 NAPVATPQ 64

RESULT 7

AH0813

probable ethanolamine utilization protein EutA eutA [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AH0813

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AH0813

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-467 <PAR>

A;Cross-references: UNIPARC:UPI0000059ADF; GB:AL513382; PIDN:CAD07690.1;

PID:g16503676; GSPDB:GN00176

C;Genetics:

A;Gene: eutA

C;Superfamily: Escherichia coli hypothetical protein b2451

Query Match 80.5%; Score 33; DB 2; Length 467;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| ||: |||
Db 338 NLPVAIPQ 345

RESULT 8

H86465

F12G12.1 protein - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: H86465

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H86465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <STO>

A;Cross-references: UNIPROT:Q9FX25; UNIPARC:UPI000009DE13; GB:AE005172;

NID:gl0086460; PIDN:AAG12520.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match	80.5%;	Score 33;	DB 2;	Length 479;
Best Local Similarity	50.0%;	Pred. No. 61;		
Matches	4;	Conservative	4;	Mismatches 0; Indels 0; Gaps 0;

Qy	1 NAPVSIPO 8
	: : : :
Db	303 NSPISVPE 310

RESULT 9

S47896

probable molybdopterin biosynthesis protein cinnamon - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C;Accession: S47896

R;Kamdar, K.P.; Shelton, M.E.; Finnerty, V.

Genetics 137, 791-801, 1994

A;Title: The *Drosophila molybdenum* cofactor gene cinnamon is homologous to three *Escherichia coli* cofactor proteins and to the rat protein gephyrin.

A;Reference number: S47896; MUID:94374679; PMID:8088525

A;Accession: S47896

A;Molecule type: mRNA

A;Residues: 1-601 <KAM>
A;Cross-references: UNIPARC:UPI000016BB49; EMBL:L19876; NID:g797288;
PIDN:AAA65877.1; PID:g505312
A;Experimental source: developmental stage embryo
C;Genetics:
A;Gene: FlyBase:cin
A;Cross-references: FlyBase:FBgn0000316
C;Function:
A;Pathway: molybdopterin biosynthesis
C;Superfamily: bifunctional molybdenum cofactor molybdenum incorporation/glycine
receptor clustering protein
C;Keywords: molybdopterin biosynthesis; multifunctional enzyme; transmembrane
protein

Query Match 80.5%; Score 33; DB 2; Length 601;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|
Db 226 NAPVNIP 232

RESULT 10

T50995
related to cytoskeleton assembly control protein SLA1 [imported] - Neurospora
crassa
N;Alternate names: protein B7F18.140
C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50995
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25286
A;Accession: T50995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1119 <SCH>
A;Cross-references: UNIPROT:Q9P3N5; UNIPARC:UPI000017B4E8; EMBL:AL389891;
GSPDB:GN00116; NCSP:B7F18.140
A;Experimental source: BAC clone B7F18; strain OR74A
C;Genetics:
A;Gene: NCSP:B7F18.140
A;Map position: 6
A;Introns: 66/3; 123/2; 495/1

Query Match 80.5%; Score 33; DB 2; Length 1119;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
||:|:|
Db 157 APISVPQ 163

RESULT 11

S16356
 ovo protein - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S16356
 R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
 EMBO J. 10, 2259-2266, 1991
 A;Title: The ovo gene of *Drosophila* encodes a zinc finger protein required for female germ line development.
 A;Reference number: S16356; MUID:91293102; PMID:1712294
 A;Accession: S16356
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1213 <MEV>
 A;Cross-references: UNIPROT:Q8T8L9; UNIPARC:UPI000017BEB1; EMBL:X59772
 C;Genetics:
 A;Gene: FlyBase:ovo
 A;Cross-references: FlyBase:FBgn0003028
 A;Introns: 931/3; 1152/3

Query Match 80.5%; Score 33; DB 2; Length 1213;
 Best Local Similarity 62.5%; Pred. No. 1.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
 |:|:|:|:
 Db 46 NSPISIPK 53

RESULT 12

T24490
 hypothetical protein T05A10.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T24490
 R;Sulston, J.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z19898
 A;Accession: T24490
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2251 <WIL>
 A;Cross-references: UNIPROT:Q22190; UNIPARC:UPI000017BB5C; EMBL:Z68108;
 PIDN:CAA92133.1; GSPDB:GN00028; CESP:T05A10.1
 A;Experimental source: clone T05A10
 C;Genetics:
 A;Gene: CESP:T05A10.1
 A;Map position: X
 A;Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2;
 1394/2; 1434/3; 1467/2; 1506/1; 1542/2; 1616/1; 1668/3; 1760/3; 1810/2; 1858/1;
 2021/3; 2055/2; 2136/3; 2184/1; 2229/3

Query Match 80.5%; Score 33; DB 2; Length 2251;
 Best Local Similarity 85.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7

||||:|
Db 1311 NAPVTIP 1317

RESULT 13

T25754

hypothetical protein F45E4.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T25754

R;Wilson, R.

submitted to the EMBL Data Library, September 1996

A;Description: The sequence of *C. elegans* cosmid F45E4.

A;Reference number: Z20082

A;Accession: T25754

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-97 <WIL>

A;Cross-references: UNIPROT:Q94228; UNIPARC:UPI000017B9CB; EMBL:U70852;

PIDN:AAB09136.1; GSPDB:GN00022; CESP:F45E4.5

A;Experimental source: strain Bristol N2; clone F45E4

C;Genetics:

A;Gene: CESP:F45E4.5

A;Map position: 4

A;Introns: 34/2; 74/1

Query Match 78.0%; Score 32; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
||| |||
Db 18 NAPAPIPQ 25

RESULT 14

AE1928

hypothetical protein all0976 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AE1928

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Iriguchi, M.; Ishikawa, A.; Kawashima, K.; Kimura, T.; Kishida, Y.; Kohara, M.;
Matsumoto, M.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.;
Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing
Cyanobacterium Anabaena sp. strain PCC 7120.

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE1928

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-249 <KUR>

A;Cross-references: UNIPROT:Q8YY75; UNIPARC:UPI00000CDF32; GB:BA000019;

PIDN:BAB72933.1; PID:g17130322; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:
A;Gene: all0976

Query Match 78.0%; Score 32; DB 2; Length 249;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | : | : |
Db 20 NAPLSVP 26

RESULT 15

AE0243

hypothetical protein YPO1996 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AE0243

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.;
Prentice, M.B.; Sebahia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker,
S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth,
T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.;
Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston,
P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Whitehead, S.; Barrell, B.G.

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AE0243

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-301 <KUR>

A;Cross-references: UNIPROT:Q8ZF00; UNIPARC:UPI00000DC6BF; GB:AL590842;

PIDN:CAC90809.1; PID:g15980010; GSPDB:GN00175

C;Genetics:

A;Gene: YPO1996

Query Match 78.0%; Score 32; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 127 NTPVSIP 133

RESULT 16

T47111

probable acetyl-CoA C-acetyltransferase (EC 2.3.1.9) [imported] - *Streptomyces* sp.

N;Alternate names: beta-ketoadipyl-CoA thiolase

C;Species: *Streptomyces* sp.

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C;Accession: T47111

R;Yang, K.; Iwagami, S.; Davies, J.E.

submitted to the EMBL Data Library, May 1999

A;Description: A protocatechuate catabolic gene cluster cloned from *Streptomyces* sp. 2065.

A;Reference number: Z24354

A;Accession: T47111

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-400 <YAN>

A;Cross-references: UNIPROT:Q9XD81; UNIPARC:UPI00000B06E6; EMBL:AF109386;
PIDN:AAD22035.1

A;Experimental source: strain 2065

C;Genetics:

A;Gene: pcaF

C;Superfamily: acetyl-CoA acetyltransferase

C;Keywords: acyltransferase; coenzyme A

Query Match 78.0%; Score 32; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
|||:||||
Db 206 APVAIPQ 212

RESULT 17

F97604

hypothetical protein AGR_C_3693 [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)

C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97604

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C58.

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97604

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-657 <KUR>

A;Cross-references: UNIPROT:Q8UDT1; UNIPARC:UPI00001643B5; GB:AE007869;
PIDN:AAK87791.1; PID:g15157164; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C_3693

A;Map position: circular chromosome

Query Match 78.0%; Score 32; DB 2; Length 657;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
||:||||
Db 148 NAAISIPQ 155

RESULT 18

AH2826

conserved hypothetical protein Atu2038 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)

C;Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AH2826

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, E.; Palmieri, A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey, S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.

A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AH2826

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-668 <KUR>

A;Cross-references: UNIPROT:Q8UDT1; UNIPARC:UPI00000D1D6C; GB:AE008688;

PIDN:AAL43030.1; PID:g17740495; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu2038

A;Map position: circular chromosome

Query Match	78.0%;	Score 32;	DB 2;	Length 668;
Best Local Similarity	75.0%;	Pred. No. 1.4e+02;		
Matches	6;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;

Qy	1 NAPVSIPQ 8
	:
Db	159 NAAISIPQ 166

RESULT 19

B70985

probable polyketide synthase - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: B70985

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70985

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1017 <COL>

A;Cross-references: UNIPROT:O06586; UNIPARC:UPI00000D5FB6; GB:Z95617;

GB:AL123456; NID:g3242249; PIDN:CAB09100.1; PID:e317264; PID:g2117231

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: pks9

C;Keywords: carrier protein

F;24-392/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>

F;504-782/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>

F;864-942/Domain: acyl carrier protein homology <ACP2>

Query Match 78.0%; Score 32; DB 2; Length 1017;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||::|
Db 412 NAPVAVP 418

RESULT 20

A43359

microtubule-associated protein MAP1A - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A43359; S22108

R;Langkopf, A.; Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.

J. Biol. Chem. 267, 16561-16566, 1992

A;Title: Microtubule-associated proteins 1A and LC2. Two proteins encoded in one messenger RNA.

A;Reference number: A43359; MUID:92355629; PMID:1379599

A;Accession: A43359

A;Molecule type: mRNA

A;Residues: 1-2774 <LAN>

A;Cross-references: UNIPROT:P34926; UNIPARC:UPI000012EBC2; GB:M83196;

NID:g205537; PIDN:AAB48069.1; PID:g205538

A;Note: sequence extracted from NCBI backbone (NCBIN:111039, NCBIP:111040)

R;Cravchik, A.

submitted to the EMBL Data Library, June 1992

A;Reference number: S22108

A;Accession: S22108

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 73-364, 'NRLRS', 370, 'QKN', 374, 'PSPKGL', 381-

751, 'RSMMSQMNAQRR', 764, 'D', 766, 'LRVPMTSL', 775, 'LKVLA', 781, 'LKPRLQIV', 807, 'FQ', 810-

811, 'R', 816, 'K', 818, 'MGHLRLN', 826, 'P', 828, 'LP', 831, 'WSPP', 836, 'WLKRNMCQPQRQSP', 851, 'V', 853, 'NSL', 855, 'LPHRWLRTN', 865, 'W', 867, 'HSQLPDGGD', 877, 'Q', 879, 'LPVARHCHEY PLFPHLK', 880-1066, 'T', 1068-1099, 'I', 1101-1488 <CRA>

A;Cross-references: UNIPARC:UPI000017752D; EMBL:X66840

A;Experimental source: strain Sprague Dawley

C;Superfamily: microtubule-associated protein MAP1B
C;Keywords: microtubule binding; phosphoprotein

Query Match 78.0%; Score 32; DB 2; Length 2774;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
|||
Db 1239 APVSIPE 1245

RESULT 21

C81662

cytosolic acyl-CoA thioester hydrolase family protein TC0822 [imported] -
Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: C81662

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: C81662

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-159 <TET>

A;Cross-references: UNIPROT:Q9PJK7; UNIPARC:UPI0000057A8C; GB:AE002348;
GB:AE002160; NID:g7190839; PIDN:AAF39624.1; PID:g7190850; GSPDB:GN00121;
TIGR:TC0822

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0822

Query Match 75.6%; Score 31; DB 2; Length 159;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:| |
Db 127 NSPVEIPE 134

RESULT 22

C83959

ribonuclease H rnh [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: C83959

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
F.; Hiramata, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: C83959

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <STO>

A;Cross-references: UNIPROT:Q9Z9S0; UNIPARC:UPI00001343BD; GB:AP001515;

GB:BA000004; NID:g10174886; PIDN:BAB06194.1; GSPDB:GN00137

A;Experimental source: strain C-125

C;Genetics:

A;Gene: rnh

C;Superfamily: ribonuclease HII

Query Match 75.6%; Score 31; DB 2; Length 263;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | : |
Db 175 NLPLSLPQ 182

RESULT 23

T35027

hypothetical protein SC4C6.19 - *Streptomyces coelicolor*

C;Species: *Streptomyces coelicolor*

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T35027

R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A;Reference number: Z21565

A;Accession: T35027

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-341 <SEE>

A;Cross-references: UNIPROT:Q9XAM1; UNIPARC:UPI00000DB17E; EMBL:AL079355;

PIDN:CAB45583.1; GSPDB:GN00070; SCOEDB:SC4C6.19

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SC4C6.19

C;Superfamily: *Streptomyces coelicolor* hypothetical protein SC4C6.19

Query Match 75.6%; Score 31; DB 2; Length 341;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 247 NAPVSAP 253

RESULT 24

AE0637

conserved hypothetical protein STY1193 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
 C;Accession: AE0637
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AE0637
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-350 <PAR>
 A;Cross-references: UNIPARC:UPI0000059FC0; GB:AL513382; PIDN:CAD08280.1; PID:g16502327; GSPDB:GN00176.
 C;Genetics:
 A;Gene: STY1193
 C;Superfamily: uncharacterized conserved protein

Query Match 75.6%; Score 31; DB 2; Length 350;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 || :||
 Db 66 NAQISVPQ 73

RESULT 25

B81194

conserved hypothetical protein NMB0471 [imported] - *Neisseria meningitidis* (strain MC58 serogroup B)

C;Species: *Neisseria meningitidis*

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: B81194

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Ketchum, K.A.; Hood, D.W.; Peden, J.F.; Dodson, R.J.; Nelson, W.C.; Gwinn, M.L.; DeBoy, R.; Peterson, J.D.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Mason, T.; Ciecko, A.; Parksey, D.S.; Blair, E.; Cittone, H.; Clark, E.B.; Cotton, M.D.; Utterback, T.R.; Khouri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, J.C.

A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: B81194

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-358 <TET>
A;Cross-references: UNIPROT:Q9K0U1; UNIPARC:UPI00000C44C1; GB:AE002404;
GB:AE002098; NID:g7225697; PIDN:AAF40908.1; PID:g7225699; GSPDB:GN00119;
TIGR:NMB0471
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0471

Query Match 75.6%; Score 31; DB 2; Length 358;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
||| |:|
Db 142 NAPASVP 148

RESULT 26

A81831

hypothetical protein NMA2014 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup A)

C;Species: *Neisseria meningitidis*

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: A81831

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morelli, G.; Basham, D.; Brown, D.; Chillingworth, T.; Davies, R.M.; Davis, P.; Devlin, K.; Feltwell, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, M.A.; Rutherford, K.M.; Simmonds, M.; Skelton, J.; Whitehead, S.; Spratt, B.G.; Barrell, B.G.
Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: A81831

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-358 <PAR>

A;Cross-references: UNIPROT:Q9JT27; UNIPARC:UPI00000C4D06; GB:AL162757;
GB:AL157959; NID:g7380371; PIDN:CAB85233.1; PID:g7380643; GSPDB:GN00124;
NMASP:NMA2014

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA2014

Query Match 75.6%; Score 31; DB 2; Length 358;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
||| |:|
Db 142 NAPASVP 148

RESULT 27

T51772

acetyl-CoA C-acetyltransferase (EC 2.3.1.9) [validated] - *Alcaligenes latus*

N;Alternate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; thiolase II
 C;Species: *Alcaligenes latus*
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C;Accession: T51772
 R;Choi, J.I.; Lee, S.Y.; Han, K.
 Appl. Environ. Microbiol. 64, 4897-4903, 1998
 A;Title: Cloning of the *Alcaligenes latus* polyhydroxyalkanoate biosynthesis genes and use of these genes for enhanced production of Poly(3-hydroxybutyrate) in *Escherichia coli*.
 A;Reference number: Z25450; MUID:99054931; PMID:9835580
 A;Accession: T51772
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-392 <CHO>
 A;Cross-references: UNIPROT:Q9ZGI9; UNIPARC:UPI00000B22B2; EMBL:AF078795; PIDN:AAC83659.1
 C;Genetics:
 A;Gene: phaA
 C;Function:
 A;Description: (EC 2.3.1.9) [validated, MUID:99054931]
 C;Superfamily: acetyl-CoA acetyltransferase
 C;Keywords: acyltransferase; coenzyme A

Query Match 75.6%; Score 31; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
 |||||
 Db 201 PVSIPQ 206

RESULT 28

C89801

hypothetical protein SA0342 [imported] - *Staphylococcus aureus* (strain N315)

C;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: C89801

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Aoki, K.; Nagai, Y.; Lian, J.; Ito, T.; Kanamori, M.; Matsumaru, H.; Maruyama, A.; Murakami, H.; Hosoyama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.; Kanehisa, M.; Yamashita, A.; Oshima, K.; Furuya, K.; Yoshino, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: C89801

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-393 <KUR>

A;Cross-references: UNIPROT:Q99WM3; UNIPARC:UPI00000CADAD; GB:BA000018;

PID:g13700268; PIDN:BAB41566.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0342

C;Superfamily: acetyl-CoA acetyltransferase

Query Match 75.6%; Score 31; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|||||
Db 201 PVSIPQ 206

RESULT 29

S72804

acetyl-CoA C-acetyltransferase (EC 2.3.1.9) atoB - Mycobacterium leprae
N;Alternate names: acetoacetyl-CoA thiolase; B1549_C1_166 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72804
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1549.
A;Reference number: S72582
A;Accession: S72804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-393 <SMI>
A;Cross-references: UNIPROT:P46707; UNIPARC:UPI0000136E44; EMBL:U00014;
NID:g466903; PIDN:AAA50881.1; PID:g466906
C;Genetics:
A;Gene: atoB
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A

Query Match 75.6%; Score 31; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|||||
Db 201 PVSIPQ 206

RESULT 30

B48376

acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Thiocystis violacea
N;Alternate names: beta-ketothiolase; poly(3-hydroxyalkanoate) synthase
C;Species: Thiocystis violacea
C;Date: 19-Nov-1993 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
C;Accession: B48376
R;Liebergessell, M.; Steinbuchel, A.
Appl. Microbiol. Biotechnol. 38, 493-501, 1993
A;Title: Cloning and molecular analysis of the poly(3-hydroxybutyric acid)
biosynthetic genes of Thiocystis violacea.
A;Reference number: A48376; MUID:93159750; PMID:7763384
A;Accession: B48376
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-394 <LIE>

A;Cross-references: UNIPARC:UPI0000175353; GB:S54369; NID:g298249;
PIDN:AAC60428.1; PID:g298251
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:124660, NCBIP:124662)
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A; ketone body metabolism; poly-beta-hydroxybutyrate biosynthesis; steroid biosynthesis
F;89/Active site: Cys #status predicted

Query Match 75.6%; Score 31; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|||
Db 202 PVSIPQ 207

RESULT 31

AG2606

conserved hypothetical protein Atu0247 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AG2606

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, E.; Palmieri, A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey, S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AG2606

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <KUR>

A;Cross-references: UNIPROT:Q8UIP6; UNIPARC:UPI00000D174D; GB:AE008688;

PIDN:AAL41269.1; PID:g17738576; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu0247

A;Map position: circular chromosome

Query Match 75.6%; Score 31; DB 2; Length 395;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| |||:
Db 249 NEPVSVPK 256

RESULT 32

F97388

probable lipase (AL392149) [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)

C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97388

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C58.

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97388

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <KUR>

A;Cross-references: UNIPROT:Q8UIP6; UNIPARC:UPI00000D174D; GB:AE007869; PIDN:AAK86063.1; PID:g15155138; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C_423

A;Map position: circular chromosome

Query Match 75.6%; Score 31; DB 2; Length 395;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| |||:|:
Db 249 NEPVSVPK 256

RESULT 33

T14728

probable betaine-aldehyde dehydrogenase (EC 1.2.1.8) - sorghum (fragment)

C;Species: *Sorghum bicolor* (sorghum)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14728

R;Wood, A.J.; Saneoka, H.; Joly, R.J.; Rhodes, D.; Goldsbrough, P.B.
Plant Physiol. 110, 1301-1308, 1996

A;Title: Betaine aldehyde dehydrogenase in *Sorghum bicolor*: molecular cloning and expression of two related genes.

A;Reference number: Z18171; MUID:97088719; PMID:8934627

A;Accession: T14728

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-424 <WOO>

A;Cross-references: UNIPROT:Q43828; UNIPARC:UPI00000AC9CD; EMBL:U12195; NID:g520543; PIDN:AAC49267.1; PID:g520544

A;Experimental source: cultivar P954035; leaf, stem

C;Function:

A;Description: catalyzes the oxidation of betaine aldehyde to betaine using NAD⁺ and water

C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

C;Keywords: NAD; oxidoreductase

Query Match 75.6%; Score 31; DB 2; Length 424;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|:|:|:|
Db 40 NSPVSLP 46

RESULT 34

D34791

interleukin-7 receptor precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C;Accession: D34791; C40256

R;Goodwin, R.G.; Friend, D.; Ziegler, S.F.; Jerzy, R.; Falk, B.A.; Gimpel, S.;
Cosman, D.; Dower, S.K.; March, C.J.; Namen, A.E.; Park, L.S.

Cell 60, 941-951, 1990

A;Title: Cloning of the human and murine interleukin-7 receptors: demonstration of a soluble form and homology to a new receptor superfamily.

A;Reference number: A34791; MUID:90199875; PMID:2317865

A;Accession: D34791

A;Molecule type: mRNA

A;Residues: 1-459 <GOO>

A;Cross-references: UNIPROT:P16872; UNIPARC:UPI0000027154; GB:M29697;

NID:g198377; PIDN:AAA39304.1; PID:g309411

R;Pleiman, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.

Mol. Cell. Biol. 11, 3052-3059, 1991

A;Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs generated by differential splicing and presence of a type I-interferon-inducible promoter.

A;Reference number: A40256; MUID:91246172; PMID:2038316

A;Accession: C40256

A;Molecule type: DNA

A;Residues: 231-239;264-272 <PLE>

A;Cross-references: UNIPARC:UPI0000176756; UNIPARC:UPI0000176757

C;Superfamily: interleukin-7 receptor; fibronectin type III repeat homology

C;Keywords: cytokine receptor; phosphoprotein; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-459/Product: interleukin-7 receptor #status predicted <MAT>

F;21-239/Domain: extracellular #status predicted <EXT>

F;240-264/Domain: transmembrane #status predicted <TMM>

Query Match 75.6%; Score 31; DB 2; Length 459;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | : | |
Db 412 NVPVPVPQ 419

RESULT 35

T16526

hypothetical protein K02F3.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T16526

R;Bentley, D.

submitted to the EMBL Data Library, May 1994

A;Description: The sequence of *C. elegans* cosmid K02F3.

A;Reference number: Z18530

A;Accession: T16526

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-504 <BEN>

A;Cross-references: UNIPARC:UPI000017BA7C; EMBL:U00052; NID:g485125;

PID:g485129; PIDN:AAA50705.1; CESP:K02F3.5

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:K02F3.5

A;Introns: 38/2; 179/3; 201/3; 271/1; 301/3; 346/1; 370/3

Query Match 75.6%; Score 31; DB 2; Length 504;

Best Local Similarity 62.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8

||| ::||

Db 360 NAPSAPVQ 367

RESULT 36

F89888

conserved hypothetical protein SA1014 [imported] - *Staphylococcus aureus* (strain N315)

C;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: F89888

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Aoki, K.; Nagai, Y.; Lian, J.; Ito, T.; Kanamori, M.; Matsumaru, H.; Maruyama, A.; Murakami, H.; Hosoyama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.; Kanehisa, M.; Yamashita, A.; Oshima, K.; Furuya, K.; Yoshino, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: F89888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-518 <KUR>

A;Cross-references: UNIPROT:Q99UT9; UNIPARC:UPI00000CACD5; GB:BA000018;

PID:g13700970; PIDN:BAB42266.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA1014

C;Superfamily: *Haemophilus influenzae* conserved hypothetical protein HI0594

Query Match 75.6%; Score 31; DB 2; Length 518;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | | | |
Db 93 NKPVSIP 99

RESULT 37

B28392

penicillin amidase (EC 3.5.1.11) I precursor - *Pseudomonas* sp.

N;Alternate names: cephalosporin acylase I

C;Species: *Pseudomonas* sp.

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: B28392

R;Matsuda, A.; Toma, K.; Komatsu, K.I.

J. Bacteriol. 169, 5821-5826, 1987

A;Title: Nucleotide sequences of the genes for two distinct cephalosporin acylases from a *Pseudomonas* strain.

A;Reference number: A91857; MUID:88058804; PMID:3680178

A;Accession: B28392

A;Molecule type: DNA

A;Residues: 1-558 <MAT>

A;Cross-references: UNIPROT:P15557; UNIPARC:UPI000016FDF1; GB:M18279;

NID:g150966; PIDN:AAA88424.1; PID:g150967

A;Experimental source: strain SE83

C;Genetics:

A;Gene: acyI

C;Superfamily: gamma-glutamyltransferase

C;Keywords: antibiotic resistance; hydrolase

Query Match 75.6%; Score 31; DB 1; Length 558;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | | : | :
Db 2 NAPVPVPR 9

RESULT 38

S27199

cephalosporin acylase - *Pseudomonas* sp. (strain V22)

C;Species: *Pseudomonas* sp.

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S27199

R;Ishiye, M.; Niwa, M.

Biochim. Biophys. Acta 1132, 233-239, 1992

A;Title: Nucleotide sequence and expression in *Escherichia coli* of the Cephalosporin acylase gene of a *Pseudomonas* strain.

A;Reference number: S27199; MUID:93041922; PMID:1358202

A;Accession: S27199

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-558 <ISH>

A;Cross-references: UNIPROT:Q05053; UNIPARC:UPI000016FDF6; EMBL:X69020;
NID:g45823; PIDN:CAA48785.1; PID:g45824
C;Superfamily: gamma-glutamyltransferase

Query Match 75.6%; Score 31; DB 2; Length 558;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
||| :|:
Db 2 NAPVPVPR 9

RESULT 39

T52163

hypothetical protein Ca49C10.19 [imported] - yeast (Candida albicans)

C;Species: Candida albicans

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52163

R;Taylor, K.; Harris, D.

submitted to the EMBL Data Library, November 1998

A;Reference number: Z25985

A;Accession: T52163

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-679 <TAY>

A;Cross-references: UNIPROT:O94033; UNIPARC:UPI0000069F51; EMBL:AL033497;

PIDN:CAA21983.1

A;Experimental source: strain 1161; cosmid Ca49C10

C;Genetics:

A;Map position: 1

A;Note: Ca49C10.19

Query Match 75.6%; Score 31; DB 2; Length 679;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | :||
Db 40 NLPTSVPQ 47

RESULT 40

T41974

replication origin binding protein (OBP) - human herpesvirus 7 (strain JI)

C;Species: human herpesvirus 7

A;Variety: strain JI

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41974

R;Nicholas, J.

submitted to the EMBL Data Library, December 1995

A;Description: Determination and analysis of the complete nucleotide sequence of human herpesvirus-7.

A;Reference number: Z22022

A;Accession: T41974

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-787 <NIC>
A;Cross-references: UNIPROT:P52379; UNIPARC:UPI0000130B96; EMBL:U43400;
PIDN:AAC54734.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U73
C;Superfamily: varicella-zoster virus gene 51 protein

Query Match 75.6%; Score 31; DB 2; Length 787;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
:|:||||
Db 353 SPISIPQ 359

RESULT 41

RGBYG4
regulatory protein GAL4 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein P1021; protein YPL248c
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A05022; S61016; S65277; S12977
R;Laughon, A.; Gesteland, R.F.
Mol. Cell. Biol. 4, 260-267, 1984
A;Title: Primary structure of the *Saccharomyces cerevisiae* GAL4 gene.
A;Reference number: A05022; MUID:84141879; PMID:6366516
A;Accession: A05022
A;Molecule type: DNA
A;Residues: 1-881 <LAU>
A;Cross-references: UNIPROT:P04386; UNIPARC:UPI0000000980; EMBL:K01486;
NID:g171557; PIDN:AAA34626.1; PID:g171558
R;Gadhavi, P.L.; Raine, A.R.C.; Alefounder, P.R.; Laue, E.D.
FEBS Lett. 276, 49-53, 1990
A;Title: Complete assignment of the (1)H NMR spectrum and secondary structure of the DNA binding domain of GAL4.
A;Reference number: S12977; MUID:91092433; PMID:2265711
A;Contents: annotation; zinc finger
R;Pohl, T.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
A;Accession: S61016
A;Molecule type: DNA
A;Residues: 1-881 <POH>
A;Cross-references: UNIPARC:UPI0000000980; EMBL:Z67751; NID:g1061234;
PIDN:CAA91596.1; PID:g1061241
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Accession: S65277
A;Molecule type: DNA
A;Residues: 1-881 <POW>
A;Cross-references: UNIPARC:UPI0000000980; EMBL:Z73604; NID:g1370510;
PIDN:CAA97969.1; PID:g1370511; GSPDB:GN00016; MIPS:YPL248c
A;Experimental source: strain S288C (AB972)

C;Comment: This protein is a positive regulator for the gene expression of the galactose-induced genes.

C;Genetics:

A;Gene: SGD:GAL4; MIPS:YPL248c

A;Cross-references: SGD:S0006169; MIPS:YPL248c

A;Map position: 16L

C;Superfamily: regulatory protein GAL4; GAL4 zinc binuclear cluster homology

C;Keywords: DNA binding; galactose utilization; transcription regulation; zinc finger

F;6-43/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F;11-38/Region: zinc finger CCCC motif

Query Match 75.6%; Score 31; DB 1; Length 881;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|:|:|:|:
Db 728 NSPVTIPR 735

RESULT 42

S57637

hexon protein - human adenovirus 4

C;Species: Mastadenovirus h4 (human adenovirus 4)

C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S57637

R;Pring-Akerblom, P.; Trijssenaar, J.; Adrian, T.

submitted to the EMBL Data Library, February 1995

A;Reference number: S57637

A;Accession: S57637

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-936 <PRI>

A;Cross-references: UNIPROT:Q67814; UNIPARC:UPI00000F2DED; EMBL:X84646;

NID:g886486; PIDN:CAA59139.1; PID:g886487

C;Superfamily: adenovirus hexon protein

Query Match 75.6%; Score 31; DB 2; Length 936;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| |:|:|
Db 646 NVPISIP 652

RESULT 43

HXAD5

hexon protein - human adenovirus 5

C;Species: Mastadenovirus h5 (human adenovirus 5)

A;Note: host Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C;Accession: A03849

R;Kinloch, R.; Mackay, N.; Mautner, V.

J. Biol. Chem. 259, 6431-6436, 1984

A;Title: Adenovirus hexon. Sequence comparison of subgroup C serotypes 2 and 5.

A;Reference number: A03849; MUID:84212465; PMID:6202684
A;Accession: A03849
A;Molecule type: DNA
A;Residues: 1-952 <KIN>
A;Cross-references: UNIPROT:P04133; UNIPARC:UPI0000170D89; GB:X02997; GB:J01966;
GB:J01980; GB:K02368; GB:V00029; GB:V00030; NID:g58498; PIDN:CAA26753.1;
PID:g58500
C;Genetics:
A;Map position: 51.6-59.7
C;Superfamily: adenovirus hexon protein
C;Keywords: hexon protein

Query Match 75.6%; Score 31; DB 1; Length 952;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| | : | | |
Db 662 NVPISIP 668

RESULT 44

HXAD2

hexon protein - human adenovirus 2 (tentative sequence)

N;Alternate names: late protein 2

C;Species: Mastadenovirus h2 (human adenovirus 2)

A;Note: host Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004

C;Accession: A94597; A92327; A93720; A03848

R;Alestrom, P.; Akusjarvi, G.; Pettersson, M.; Pettersson, U.
submitted to the Atlas, November 1982

A;Reference number: A94597

A;Contents: revisions

A;Accession: A94597

A;Molecule type: DNA

A;Residues: 145-165;450-457 <ALE>

A;Cross-references: UNIPROT:P03277; UNIPARC:UPI00001749C2; UNIPARC:UPI00001749C3
R;Jornvall, H.; Akusjarvi, G.; Alestrom, P.; von Bahr-Lindstrom, H.; Pettersson,
U.; Appella, E.; Fowler, A.V.; Philipson, L.

J. Biol. Chem. 256, 6181-6186, 1981

A;Title: The adenovirus hexon protein. The primary structure of the polypeptide
and its correlation with the hexon gene.

A;Reference number: A92327; MUID:81215564; PMID:6263909

A;Accession: A92327

A;Molecule type: protein

A;Residues: 1-454;456-967 <JOR>

A;Cross-references: UNIPARC:UPI00001749C4; UNIPARC:UPI00001749C5

A;Note: this is the final paper of a series giving the experimental details

A;Note: sequences of residues 1-101, 239-261, 275-301, 317-325, 329-364, 501-
525, 529-550, 612-628, and 800-967 were confirmed by the corresponding
nucleotide sequences

A;Note: the sequences of residues 146-159 and 234-235 were assigned based on
preliminary data

R;Akusjarvi, G.; Zabielski, J.; Perricaudet, M.; Pettersson, U.

Nucleic Acids Res. 9, 1-17, 1981

A;Title: The sequence of the 3' non-coding region of the hexon mRNA discloses a
novel adenovirus gene.

A;Reference number: A93720; MUID:81150446; PMID:6259616
A;Accession: A93720
A;Molecule type: DNA
A;Residues: 922-966 <AKU>
A;Cross-references: UNIPARC:UPI00001749C6
C;Comment: This protein is one of the structural proteins in the viral coat and is synthesized during late infection.
C;Genetics:
A;Map position: 51.7-61.3
C;Superfamily: adenovirus hexon protein
C;Keywords: acetylated amino end; coat protein; hexon protein; late protein
F;1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 75.6%; Score 31; DB 1; Length 967;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| :|||
Db 677 NVPISIP 683

RESULT 45

E70751

probable nrp protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: E70751

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: E70751

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-2512 <COL>

A;Cross-references: UNIPROT:Q10896; UNIPARC:UPI00000D5046; GB:Z74410;

GB:AL123456; NID:g3261600; PIDN:CAA98937.1; PID:e249456; PID:g1405772

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: nrp

C;Keywords: carrier protein; phosphopantetheine; phosphoprotein

F;479-915/Domain: acetate-CoA ligase homology <ACL1>

F;1538-1971/Domain: acetate-CoA ligase homology <ACL>

F;1987-2055/Domain: acyl carrier protein homology <ACP>

F;2019/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 75.6%; Score 31; DB 2; Length 2512;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8
|||
Db 1491 PVSIPQ 1496

RESULT 46

T49799

related to TOM1 protein [imported] - *Neurospora crassa*

N;Alternate names: protein B11B22.10

C;Species: *Neurospora crassa*

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T49799

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.

submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49799

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-3839 <SCH>

A;Cross-references: UNIPROT:Q9P4Z1; UNIPARC:UPI000017B515; EMBL:AL356834;

GSPDB:GN00116; NCSP:B11B22.10

A;Experimental source: BAC clone B11B22; strain OR74A

C;Genetics:

A;Gene: NCSP:B11B22.10

A;Map position: 6

A;Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1

Query Match 75.6%; Score 31; DB 2; Length 3839;
Best Local Similarity 85.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|
Db 743 NRPVSIP 749

RESULT 47

S06675

apidaecin Ib precursor - honeybee

C;Species: *Apis mellifera* (honeybee)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: S06675

R;Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989

A;Title: Apidaecins: antibacterial peptides from honeybees.

A;Reference number: S05383; MUID:90005446; PMID:2676519

A;Accession: S06675

A;Molecule type: protein

A;Residues: 1-26 <CAS>

A;Cross-references: UNIPROT:Q06602; UNIPARC:UPI000017BF09

F;1-8/Domain: propeptide #status experimental <PRO>

F;9-26/Product: apidaecin Ib #status experimental <MAT>

Query Match 73.2%; Score 30; DB 2; Length 26;

Best Local Similarity 75.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | |
Db 11 NRPVYIPQ 18

RESULT 48

AE0106

conserved hypothetical protein YPO0866 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AE0106

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AE0106

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <KUR>

A;Cross-references: UNIPROT:Q8ZHM5; UNIPARC:UPI00000DCACC; GB:AL590842;

PIDN:CAC89712.1; PID:gl5978939; GSPDB:GN00175

C;Genetics:

A;Gene: YPO0866

Query Match 73.2%; Score 30; DB 2; Length 101;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | |
Db 48 NDPVSCPQ 55

RESULT 49

A22706

vitelline membrane protein - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997

C;Accession: A22706

R;Mindrinos, M.N.; Scherer, L.J.; Garcini, F.J.; Kwan, H.; Jacobs, K.A.; Petri, W.H.

EMBO J. 4, 147-153, 1985

A;Title: Isolation and chromosomal location of putative vitelline membrane genes in *Drosophila melanogaster*.

A;Reference number: A22706; MUID:85257433; PMID:3926479

A;Contents: Plasmid DmcMM99

A;Accession: A22706

A;Molecule type: mRNA
A;Residues: 1-104 <MIN>
A;Cross-references: UNIPARC:UPI000017BEE7
C;Genetics:
A;Gene: FlyBase:Vm34Ca
A;Cross-references: FlyBase:FBgn0003983
C;Keywords: membrane protein

Query Match 73.2%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIP 7
|||
Db 74 APVSIP 79

RESULT 50

F64700

biopolymer transport protein - Helicobacter pylori

C;Species: Helicobacter pylori

A;Variety: strains J99, 26695

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: F64700; A71821

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald,
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;
Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;
Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter
pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: F64700

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-133 <TOM>

A;Cross-references: UNIPROT:O25987; UNIPARC:UPI000012A350; GB:AE000644;

GB:AE000511; NID:g2314609; PIDN:AAD08484.1; PID:g2314618; TIGR:HP1446

A;Experimental source: strain 26695

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.;
Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.;
Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: A71821

A;Molecule type: DNA

A;Residues: 1-133 <ARN>

A;Cross-references: UNIPARC:UPI000012A350; GB:AE001556; GB:AE001439;

NID:g4155938; PIDN:AAD06915.1; PID:g4155949

A;Experimental source: strain J99

C;Genetics:

A;Gene: exbD_3

A;Start codon: GTG

C;Superfamily: tolR protein

Query Match 73.2%; Score 30; DB 2; Length 133;

Best Local Similarity 83.3%; Pred. No. 60;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PVSIPQ 8

|:||||

Db 36 PISIPQ 41

Search completed: April 26, 2006, 00:22:48

Job time : 67 secs

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OM protein - protein search, using sw model

Run on: April 26, 2006, 00:23:02 ; Search time 164 Seconds
 (without alignments)
 20.382 Million cell updates/sec

Title: US-10-748-765-2
 Perfect score: 41
 Sequence: 1 NAPVSIPQ 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	41	100.0	8	3	US-09-267-511-2	Sequence 2, Appli
2	41	100.0	8	4	US-10-164-432-4	Sequence 4, Appli
3	41	100.0	8	4	US-10-296-849-2	Sequence 2, Appli
4	41	100.0	8	4	US-10-623-272-6	Sequence 6, Appli
5	41	100.0	8	5	US-10-748-765-2	Sequence 2, Appli
6	41	100.0	8	5	US-10-489-515-13	Sequence 13, Appl
7	41	100.0	10	3	US-09-267-511-23	Sequence 23, Appl
8	41	100.0	10	4	US-10-296-849-20	Sequence 20, Appl
9	41	100.0	10	4	US-10-623-272-33	Sequence 33, Appl
10	41	100.0	10	5	US-10-748-765-9	Sequence 9, Appli
11	41	100.0	13	3	US-09-267-511-24	Sequence 24, Appl

12	41	100.0	13	4	US-10-296-849-21	Sequence 21, Appl
13	41	100.0	13	4	US-10-623-272-34	Sequence 34, Appl
14	41	100.0	13	5	US-10-748-765-10	Sequence 10, Appl
15	41	100.0	15	3	US-09-267-511-25	Sequence 25, Appl
16	41	100.0	15	4	US-10-296-849-22	Sequence 22, Appl
17	41	100.0	15	4	US-10-623-272-35	Sequence 35, Appl
18	41	100.0	15	5	US-10-748-765-11	Sequence 11, Appl
19	41	100.0	17	3	US-09-267-511-19	Sequence 19, Appl
20	41	100.0	17	3	US-09-267-511-26	Sequence 26, Appl
21	41	100.0	18	3	US-09-267-511-18	Sequence 18, Appl
22	41	100.0	18	3	US-09-267-511-20	Sequence 20, Appl
23	41	100.0	18	4	US-10-296-849-23	Sequence 23, Appl
24	41	100.0	18	4	US-10-623-272-12	Sequence 12, Appl
25	41	100.0	18	5	US-10-748-765-12	Sequence 12, Appl
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27	41	100.0	88	4	US-10-296-849-13	Sequence 13, Appl
28	41	100.0	88	4	US-10-623-272-10	Sequence 10, Appl
29	41	100.0	88	5	US-10-748-765-14	Sequence 14, Appl
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33	41	100.0	800	4	US-10-623-272-41	Sequence 41, Appl
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35	41	100.0	828	4	US-10-623-272-55	Sequence 55, Appl
36	41	100.0	874	4	US-10-623-272-59	Sequence 59, Appl
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38	41	100.0	1102	3	US-09-364-609-8	Sequence 8, Appli
39	41	100.0	1102	4	US-10-164-432-2	Sequence 2, Appli
40	41	100.0	1102	4	US-10-221-625-49	Sequence 49, Appl
41	36	87.8	9	4	US-10-623-272-28	Sequence 28, Appl
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45	36	87.8	510	4	US-10-282-122A-74577	Sequence 74577, A
46	36	87.8	510	6	US-11-144-352-18	Sequence 18, Appl
47	36	87.8	511	4	US-10-282-122A-72068	Sequence 72068, A
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60	33	80.5	344	3	US-09-808-387-12	Sequence 12, Appl
61	33	80.5	344	3	US-09-808-387-18	Sequence 18, Appl
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63	33	80.5	386	3	US-09-808-387-6	Sequence 6, Appli
64	33	80.5	386	5	US-10-746-547-30	Sequence 30, Appl
65	33	80.5	479	4	US-10-412-699B-630	Sequence 630, App
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67	33	80.5	520	4	US-10-437-963-179595	Sequence 179595,
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71	33	80.5	574	3	US-09-808-387-8	Sequence 8, Appli
72	33	80.5	574	3	US-09-808-387-16	Sequence 16, Appl
73	33	80.5	574	5	US-10-756-149-5324	Sequence 5324, Ap
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79	32	78.0	179	4	US-10-767-701-51200	Sequence 51200, A
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87	31	75.6	55	4	US-10-425-115-368976	Sequence 368976,
88	31	75.6	69	3	US-09-864-761-34136	Sequence 34136, A
89	31	75.6	69	4	US-10-425-115-363068	Sequence 363068,
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94	31	75.6	123	4	US-10-425-115-189292	Sequence 189292,
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96	31	75.6	159	4	US-10-282-122A-55313	Sequence 55313, A
97	31	75.6	174	4	US-10-369-493-9670	Sequence 9670, Ap
98	31	75.6	194	4	US-10-156-761-14036	Sequence 14036, A
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117	31	75.6	433	4	US-10-282-122A-59137	Sequence 59137, A
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122	31	75.6	518	5	US-10-470-048B-331	Sequence 331, App
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126	31	75.6	573	4	US-10-374-780A-2784	Sequence 2784, Ap
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136	31	75.6	881	5	US-10-888-313A-55	Sequence 55, Appl
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175	30	73.2	55	4	US-10-264-049-3293	Sequence 3293, Ap
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258	30	73.2	367	4	US-10-341-434-93	Sequence 93, Appl
259	30	73.2	367	5	US-10-491-545A-45	Sequence 45, Appl
260	30	73.2	367	5	US-10-631-467-848	Sequence 848, App
261	30	73.2	367	5	US-10-631-467-1568	Sequence 1568, Ap
262	30	73.2	384	5	US-10-739-930-8959	Sequence 8959, Ap
263	30	73.2	395	4	US-10-282-122A-74673	Sequence 74673, A
264	30	73.2	398	5	US-10-732-923-23423	Sequence 23423, A
265	30	73.2	411	4	US-10-335-977-9493	Sequence 9493, Ap
266	30	73.2	414	5	US-10-450-763-39226	Sequence 39226, A
267	30	73.2	416	5	US-10-450-763-53325	Sequence 53325, A
268	30	73.2	427	5	US-10-732-923-11648	Sequence 11648, A
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271	30	73.2	442	4	US-10-425-114-63973	Sequence 63973, A
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275	30	73.2	463	4	US-10-437-963-152710	Sequence 152710,
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277	30	73.2	480	5	US-10-783-528-96	Sequence 96, Appl
278	30	73.2	485	5	US-10-732-923-23848	Sequence 23848, A
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282	30	73.2	488	4	US-10-295-027-1326	Sequence 1326, Ap
283	30	73.2	488	4	US-10-755-889-170	Sequence 170, App
284	30	73.2	488	5	US-10-925-095-561	Sequence 561, App
285	30	73.2	488	5	US-10-688-790-18	Sequence 18, Appl
286	30	73.2	490	4	US-10-243-501-3	Sequence 3, Appli
287	30	73.2	490	4	US-10-243-351-2	Sequence 2, Appli
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303	30	73.2	815	4	US-10-372-054-26	Sequence 26, Appl
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305	30	73.2	821	4	US-10-376-564-33	Sequence 33, Appl
306	30	73.2	825	5	US-10-631-467-779	Sequence 779, App
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309	30	73.2	829	3	US-09-975-723A-1	Sequence 1, Appli
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311	30	73.2	829	4	US-10-174-677-21	Sequence 21, Appl
312	30	73.2	829	4	US-10-158-123-1	Sequence 1, Appli
313	30	73.2	829	4	US-10-295-027-338	Sequence 338, App
314	30	73.2	829	4	US-10-295-027-783	Sequence 783, App
315	30	73.2	829	4	US-10-295-027-800	Sequence 800, App
316	30	73.2	829	4	US-10-295-027-863	Sequence 863, App
317	30	73.2	829	4	US-10-295-027-896	Sequence 896, App
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322	30	73.2	829	4	US-10-274-177-16	Sequence 16, Appl
323	30	73.2	829	4	US-10-650-112-16	Sequence 16, Appl
324	30	73.2	829	4	US-10-712-124-86	Sequence 86, Appl
325	30	73.2	829	5	US-10-643-795A-145	Sequence 145, App
326	30	73.2	829	5	US-10-678-160A-6	Sequence 6, Appli
327	30	73.2	829	5	US-10-723-860-2835	Sequence 2835, Ap
328	30	73.2	829	5	US-10-696-639-39	Sequence 39, Appl
329	30	73.2	829	5	US-10-948-518-145	Sequence 145, App
330	30	73.2	829	5	US-10-756-149-5498	Sequence 5498, Ap
331	30	73.2	829	6	US-11-037-713-22	Sequence 22, Appl
332	30	73.2	829	6	US-11-041-788-16	Sequence 16, Appl
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336	30	73.2	946	3	US-09-953-280-44	Sequence 44, Appl
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348	29	70.7	18	3	US-09-912-609-48	Sequence 48, Appl
349	29	70.7	18	4	US-10-277-232-160	Sequence 160, App
350	29	70.7	18	4	US-10-277-233-160	Sequence 160, App
351	29	70.7	18	5	US-10-838-289-681	Sequence 681, App
352	29	70.7	23	5	US-10-492-928A-18	Sequence 18, Appl
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358	29	70.7	72	4	US-10-424-599-255612	Sequence 255612,
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362	29	70.7	83	4	US-10-437-963-122227	Sequence 122227,
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364	29	70.7	95	4	US-10-106-698-5528	Sequence 5528, Ap
365	29	70.7	99	4	US-10-424-599-164847	Sequence 164847,
366	29	70.7	101	4	US-10-425-115-187987	Sequence 187987,
367	29	70.7	102	3	US-09-764-875-630	Sequence 630, App
368	29	70.7	108	4	US-10-106-698-4288	Sequence 4288, Ap
369	29	70.7	112	4	US-10-424-599-188372	Sequence 188372,
370	29	70.7	112	4	US-10-425-115-356329	Sequence 356329,
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372	29	70.7	122	4	US-10-437-963-168153	Sequence 168153,
373	29	70.7	129	4	US-10-767-701-40009	Sequence 40009, A
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378	29	70.7	154	3	US-09-864-761-34493	Sequence 34493, A
379	29	70.7	162	4	US-10-424-599-164577	Sequence 164577,
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384	29	70.7	178	4	US-10-425-115-279701	Sequence 279701,
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387	29	70.7	180	4	US-10-335-977-5735	Sequence 5735, Ap
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396	29	70.7	201	4	US-10-767-701-60720	Sequence 60720, A
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403	29	70.7	236	4	US-10-335-977-6778	Sequence 6778, Ap
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408	29	70.7	254	4	US-10-371-264-63	Sequence 63, Appl
409	29	70.7	254	4	US-10-371-099-358	Sequence 358, App
410	29	70.7	254	4	US-10-371-099-359	Sequence 359, App

411	29	70.7	254	4	US-10-371-122-358	Sequence 358, App
412	29	70.7	254	4	US-10-371-122-359	Sequence 359, App
413	29	70.7	254	4	US-10-373-567-62	Sequence 62, Appl
414	29	70.7	254	4	US-10-373-567-63	Sequence 63, Appl
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416	29	70.7	254	4	US-10-628-088-359	Sequence 359, App
417	29	70.7	254	5	US-10-831-780-358	Sequence 358, App
418	29	70.7	254	5	US-10-831-780-359	Sequence 359, App
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420	29	70.7	254	5	US-10-466-811-32	Sequence 32, Appl
421	29	70.7	254	5	US-10-831-781-62	Sequence 62, Appl
422	29	70.7	254	5	US-10-831-781-63	Sequence 63, Appl
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431	29	70.7	291	4	US-10-437-963-156836	Sequence 156836,
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438	29	70.7	338	5	US-10-739-930-10450	Sequence 10450, A
439	29	70.7	344	4	US-10-369-493-13401	Sequence 13401, A
440	29	70.7	349	6	US-11-097-143-15978	Sequence 15978, A
441	29	70.7	359	4	US-10-369-493-3818	Sequence 3818, Ap
442	29	70.7	384	4	US-10-425-115-299079	Sequence 299079,
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445	29	70.7	395	3	US-09-932-367A-4	Sequence 4, Appli
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453	29	70.7	440	4	US-10-448-871A-14	Sequence 14, Appl
454	29	70.7	440	4	US-10-448-871A-15	Sequence 15, Appl
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457	29	70.7	449	4	US-10-074-475-272	Sequence 272, App
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462	29	70.7	469	5	US-10-473-753-23	Sequence 23, Appl
463	29	70.7	469	5	US-10-473-753-24	Sequence 24, Appl
464	29	70.7	469	5	US-10-473-753-25	Sequence 25, Appl
465	29	70.7	473	4	US-10-369-493-4448	Sequence 4448, Ap
466	29	70.7	483	4	US-10-369-493-7207	Sequence 7207, Ap
467	29	70.7	493	4	US-10-425-115-348574	Sequence 348574,

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489	29	70.7	602	4	US-10-225-066A-546	Sequence 546, App
490	29	70.7	602	4	US-10-302-267-102	Sequence 102, App
491	29	70.7	602	4	US-10-374-780A-2400	Sequence 2400, Ap
492	29	70.7	602	4	US-10-437-963-195456	Sequence 195456,
493	29	70.7	602	5	US-10-739-930-5686	Sequence 5686, Ap
494	29	70.7	602	5	US-10-225-066A-546	Sequence 546, App
495	29	70.7	608	6	US-11-097-143-19626	Sequence 19626, A
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508	29	70.7	805	6	US-11-097-143-26394	Sequence 26394, A
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517	29	70.7	895	6	US-11-097-143-17049	Sequence 17049, A
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519	29	70.7	983	4	US-10-112-944-435	Sequence 435, App
520	29	70.7	985	6	US-11-097-143-17463	Sequence 17463, A
521	29	70.7	985	6	US-11-097-143-27048	Sequence 27048, A
522	29	70.7	1014	4	US-10-437-963-106652	Sequence 106652,
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535	29	70.7	1278	6	US-11-097-143-42438	Sequence 42438, A
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543	29	70.7	1390	6	US-11-050-926-35	Sequence 35, Appl
544	29	70.7	1454	4	US-10-408-765A-1328	Sequence 1328, Ap
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552	29	70.7	2073	4	US-10-742-350-15	Sequence 15, Appl
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554	29	70.7	2141	4	US-10-014-814-6	Sequence 6, Appli
555	29	70.7	2141	5	US-10-690-276-10	Sequence 10, Appl
556	29	70.7	2193	5	US-10-490-592-5	Sequence 5, Appli
557	29	70.7	2245	4	US-10-618-941-108	Sequence 108, App
558	29	70.7	2376	4	US-10-144-194A-72	Sequence 72, Appl
559	29	70.7	2376	5	US-10-491-566-72	Sequence 72, Appl
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677	28	68.3	254	5	US-10-831-780-360	Sequence 360, App
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680	28	68.3	254	5	US-10-466-811-97	Sequence 97, Appl
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ALIGNMENTS

RESULT 1

US-09-267-511-2

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; Sequence 2, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:activity
;   OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
;   OTHER INFORMATION: active site
US-09-267-511-2

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Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 NAPVSIPQ 8

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US-10-164-432-4

; Sequence 4, Application US/10164432
; Publication No. US20030166544A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Inc.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Debra, Shade L.
; TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic Neuropathy
; FILE REFERENCE: 1975A US
; CURRENT APPLICATION NUMBER: US/10/164,432
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/921,029
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/230,964
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-164-432-4

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
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US-10-296-849-2

; Sequence 2, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory

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; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Activity
;   OTHER INFORMATION: Dependent Neurotrophic Factor III (ADNF III)
;   OTHER INFORMATION: active core site, NAP or ADNF III-8
US-10-296-849-2

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; Sequence 6, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III-8
; OTHER INFORMATION: active site core peptide, clone 25 sequence (NAP)
US-10-623-272-6

Query Match 100.0%; Score 41; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

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; Sequence 2, Application US/10748765
; Publication No. US20040235747A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Offen, Daniel
; APPLICANT: Giladi, Eliezer
; APPLICANT: Melamed, Eldad
; APPLICANT: Brenneman, Douglas
; APPLICANT: Ramot at Tel-Aviv University, Ltd.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 019856-000210US
; CURRENT APPLICATION NUMBER: US/10/748,765
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,650
; PRIOR FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
; OTHER INFORMATION: active core site (NAP)
US-10-748-765-2

Query Match 100.0%; Score 41; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 1 NAPVSIPQ 8

RESULT 6

US-10-489-515-13

; Sequence 13, Application US/10489515
 ; Publication No. US20050054837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenneman, Douglas E.
 ; APPLICANT: Castellon, Raquel
 ; APPLICANT: Spong, Catherine Y.
 ; APPLICANT: Hauser, Janet M.
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by The Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; APPLICANT: Ramot University Authority for Applied Research
 ; APPLICANT: and Industrial Development, Ltd.
 ; TITLE OF INVENTION: Neurotrophic Components of the ADNF I Complex
 ; FILE REFERENCE: 15280W-005200US
 ; CURRENT APPLICATION NUMBER: US/10/489,515
 ; CURRENT FILING DATE: 2004-03-11
 ; PRIOR APPLICATION NUMBER: US 60/322,760
 ; PRIOR FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US 60/371,961
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: WO PCT/US02/29146
 ; PRIOR FILING DATE: 2002-09-12
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Activity
 ; OTHER INFORMATION: Dependent Neuroprotective Protein (ADNP or ADNF
 ; OTHER INFORMATION: III) active core site, NAP
 US-10-489-515-13

Query Match 100.0%; Score 41; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 1 NAPVSIPQ 8

RESULT 7

US-09-267-511-23

; Sequence 23, Application US/09267511
 ; Patent No. US20020111301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenneman, Douglas E.
 ; APPLICANT: Spong, Catherine Y.
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: Bassan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America

```

; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-267-511-23

```

```

Query Match          100.0%; Score 41; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      3 NAPVSIPQ 10

```

RESULT 8

US-10-296-849-20

```

; Sequence 20, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 10
;   TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-296-849-20

Query Match 100.0%; Score 41; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 3 NAPVSIPQ 10

RESULT 9

US-10-623-272-33

; Sequence 33, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-623-272-33

Query Match 100.0%; Score 41; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 3 NAPVSIPQ 10

RESULT 10

US-10-748-765-9

; Sequence 9, Application US/10748765
 ; Publication No. US20040235747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: Offen, Daniel
 ; APPLICANT: Giladi, Eliezer
 ; APPLICANT: Melamed, Eldad
 ; APPLICANT: Brenneman, Douglas
 ; APPLICANT: Ramot at Tel-Aviv University, Ltd.
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by The Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
 ; TITLE OF INVENTION: Diseases
 ; FILE REFERENCE: 019856-000210US
 ; CURRENT APPLICATION NUMBER: US/10/748,765
 ; CURRENT FILING DATE: 2003-12-29
 ; PRIOR APPLICATION NUMBER: US 60/437,650
 ; PRIOR FILING DATE: 2003-01-02
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
 ; OTHER INFORMATION: polypeptide

US-10-748-765-9

Query Match 100.0%; Score 41; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 3 NAPVSIPQ 10

RESULT 11

US-09-267-511-24

; Sequence 24, Application US/09267511
 ; Patent No. US20020111301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenneman, Douglas E.
 ; APPLICANT: Spong, Catherine Y.
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: Bassan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; APPLICANT: Ramot University Authority for Applied Research
 ; APPLICANT: and Industrial Development, Ltd.
 ; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell

; TITLE OF INVENTION: Death With ADNF Polypeptides
 ; FILE REFERENCE: 015280-377000US
 ; CURRENT APPLICATION NUMBER: US/09/267,511
 ; CURRENT FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
 ; OTHER INFORMATION: polypeptide
 US-09-267-511-24

Query Match 100.0%; Score 41; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 4 NAPVSIPQ 11

RESULT 12

US-10-296-849-21
 ; Sequence 21, Application US/10296849
 ; Publication No. US20040048801A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Spong, Catherine Y.
 ; APPLICANT: Brenneman, Douglas
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; APPLICANT: Ramot University Authority for Applied and
 ; APPLICANT: Industrial Development, Ltd.
 ; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
 ; FILE REFERENCE: 15280W-004200US
 ; CURRENT APPLICATION NUMBER: US/10/296,849
 ; CURRENT FILING DATE: 2003-06-18
 ; PRIOR APPLICATION NUMBER: US 60/208,944
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: US 60/267,805
 ; PRIOR FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
 ; PRIOR FILING DATE: 2001-05-31
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
 ; OTHER INFORMATION: polypeptide
 US-10-296-849-21

Query Match 100.0%; Score 41; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||||
Db 4 NAPVSIPQ 11

RESULT 13

US-10-623-272-34

; Sequence 34, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide

US-10-623-272-34

Query Match 100.0%; Score 41; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||||
Db 4 NAPVSIPQ 11

RESULT 14

US-10-748-765-10

; Sequence 10, Application US/10748765
; Publication No. US20040235747A1
; GENERAL INFORMATION:

```

; APPLICANT: Gozes, Illana
; APPLICANT: Offen, Daniel
; APPLICANT: Giladi, Eliezer
; APPLICANT: Melamed, Eldad
; APPLICANT: Brenneman, Douglas
; APPLICANT: Ramot at Tel-Aviv University, Ltd.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 019856-000210US
; CURRENT APPLICATION NUMBER: US/10/748,765
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,650
; PRIOR FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-748-765-10

```

```

Query Match          100.0%; Score 41; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      4 NAPVSIPQ 11

```

RESULT 15

US-09-267-511-25

```

; Sequence 25, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-25

Query Match 100.0%; Score 41; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||||
Db 6 NAPVSIPQ 13

RESULT 16

US-10-296-849-22

; Sequence 22, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-296-849-22

Query Match 100.0%; Score 41; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||||
Db 6 NAPVSIPQ 13

RESULT 17

US-10-623-272-35

; Sequence 35, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-623-272-35

Query Match 100.0%; Score 41; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||||
Db 6 NAPVSIPQ 13

RESULT 18

US-10-748-765-11

; Sequence 11, Application US/10748765
; Publication No. US20040235747A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Offen, Daniel
; APPLICANT: Giladi, Eliezer
; APPLICANT: Melamed, Eldad
; APPLICANT: Brenneman, Douglas

```

; APPLICANT: Ramot at Tel-Aviv University, Ltd.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 019856-000210US
; CURRENT APPLICATION NUMBER: US/10/748,765
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,650
; PRIOR FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-748-765-11

```

```

Query Match          100.0%; Score 41; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      6 NAPVSIPQ 13

```

RESULT 19

US-09-267-511-19

```

; Sequence 19, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-19

Query Match 100.0%; Score 41; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 6 NAPVSIPQ 13

RESULT 20

US-09-267-511-26

; Sequence 26, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-26

Query Match 100.0%; Score 41; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 8 NAPVSIPQ 15

RESULT 21

US-09-267-511-18

; Sequence 18, Application US/09267511

```

; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-09-267-511-18

```

```

Query Match          100.0%; Score 41; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      6 NAPVSIPQ 13

```

RESULT 22

```

US-09-267-511-20
; Sequence 20, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12

```

```
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-09-267-511-20
```

```
Query Match          100.0%; Score 41; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      6 NAPVSIPQ 13
```

RESULT 23

```
US-10-296-849-23
; Sequence 23, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-296-849-23
```

```
Query Match          100.0%; Score 41; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

Qy 1 NAPVSIPQ 8
|||
Db 9 NAPVSIPQ 16

RESULT 24

US-10-623-272-12
; Sequence 12, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
US-10-623-272-12

Query Match 100.0%; Score 41; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 9 NAPVSIPQ 16

RESULT 25

US-10-748-765-12
; Sequence 12, Application US/10748765
; Publication No. US20040235747A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Offen, Daniel
; APPLICANT: Giladi, Eliezer
; APPLICANT: Melamed, Eldad

```

; APPLICANT: Brenneman, Douglas
; APPLICANT: Ramot at Tel-Aviv University, Ltd.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 019856-000210US
; CURRENT APPLICATION NUMBER: US/10/748,765
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,650
; PRIOR FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ADNF III
;   OTHER INFORMATION: polypeptide
US-10-748-765-12

```

```

Query Match          100.0%; Score 41; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      9 NAPVSIPQ 16

```

RESULT 26

US-09-267-511-4

```

; Sequence 4, Application US/09267511
; Patent No. US20020111301A1
; GENERAL INFORMATION:
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Gozes, Illana
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied Research
; APPLICANT: and Industrial Development, Ltd.
; TITLE OF INVENTION: Prevention of Fetal Alcohol Syndrome and Neuronal Cell
; TITLE OF INVENTION: Death With ADNF Polypeptides
; FILE REFERENCE: 015280-377000US
; CURRENT APPLICATION NUMBER: US/09/267,511
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 88
;   TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF I
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may
; OTHER INFORMATION: be present or absent

```

US-09-267-511-4

```

Query Match          100.0%; Score 41; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      41 NAPVSIPQ 48

```

RESULT 27

US-10-296-849-13

```

; Sequence 13, Application US/10296849
; Publication No. US20040048801A1
; GENERAL INFORMATION:
; APPLICANT: Spong, Catherine Y.
; APPLICANT: Brenneman, Douglas
; APPLICANT: Gozes, Illana
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Ramot University Authority for Applied and
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Use of ADNF for Enhancing Learning and Memory
; FILE REFERENCE: 15280W-004200US
; CURRENT APPLICATION NUMBER: US/10/296,849
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/208,944
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 60/267,805
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: WO PCT/US01/17758
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Activity
; OTHER INFORMATION: Dependent Neurotrophic Factor III (ADNF III)

```



```

; OTHER INFORMATION: polypeptide formula
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, may be present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, may be present or absent
US-10-296-849-13

```

```

Query Match          100.0%; Score 41; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      41 NAPVSIPQ 48

```

RESULT 28

US-10-623-272-10

```

; Sequence 10, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:activity
; OTHER INFORMATION: dependent neurotrophic factor III (ADNF III)
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-40 may be
; OTHER INFORMATION: present or absent

```

; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 49-88 may be
; OTHER INFORMATION: present or absent
US-10-623-272-10

Query Match 100.0%; Score 41; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 41 NAPVSIPQ 48

RESULT 29

US-10-748-765-14

; Sequence 14, Application US/10748765
; Publication No. US20040235747A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Offen, Daniel
; APPLICANT: Giladi, Eliezer
; APPLICANT: Melamed, Eldad
; APPLICANT: Brenneman, Douglas
; APPLICANT: Ramot at Tel-Aviv University, Ltd.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods of Treating and/or Preventing Autoimmune
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 019856-000210US
; CURRENT APPLICATION NUMBER: US/10/748,765
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/437,650
; PRIOR FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ADNF III
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(40)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid or known
; OTHER INFORMATION: analogue of a natural amino acid, Xaa at positions
; OTHER INFORMATION: 1-40 may be present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (49)..(88)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid or known
; OTHER INFORMATION: analogue of a natural amino acid, Xaa at positions

; OTHER INFORMATION: 49-88 may be present or absent
US-10-748-765-14

Query Match 100.0%; Score 41; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
|||
Db 41 NAPVSIPO 48

RESULT 30

US-10-623-272-57

; Sequence 57, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-272-57

Query Match 100.0%; Score 41; DB 4; Length 726;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
|||
Db 59 NAPVSIPO 66

RESULT 31

US-10-623-272-32

; Sequence 32, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana

```

; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 781
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human activity dependent neurotrophic factor III
;   OTHER INFORMATION: (ADNF III)
US-10-623-272-32

```

```

Query Match          100.0%;  Score 41;  DB 4;  Length 781;
Best Local Similarity 100.0%;  Pred. No. 50;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 NAPVSIPQ 8
             |||||
Db          33 NAPVSIPQ 40

```

RESULT 32

```

US-10-623-272-31
; Sequence 31, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485

```

```
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III)
US-10-623-272-31
```

```
Query Match          100.0%; Score 41; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 50;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      33 NAPVSIPQ 40
```

```
RESULT 33
US-10-623-272-41
; Sequence 41, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(800)
; OTHER INFORMATION: translation of H3' human ADNF III cDNA clone
US-10-623-272-41
```

```
Query Match          100.0%; Score 41; DB 4; Length 800;
Best Local Similarity 100.0%; Pred. No. 51;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 52 NAPVSIPQ 59

RESULT 34

US-10-623-272-3

; Sequence 3, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse activity dependent neurotrophic factor III
; OTHER INFORMATION: (ADNF III) cDNA clone
US-10-623-272-3

Query Match 100.0%; Score 41; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 52 NAPVSIPQ 59

RESULT 35

US-10-623-272-55

; Sequence 55, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav

```

; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-623-272-55

```

```

Query Match          100.0%; Score 41; DB 4; Length 828;
Best Local Similarity 100.0%; Pred. No. 53;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      74 NAPVSIPQ 81

```

RESULT 36

```

US-10-623-272-59
; Sequence 59, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 874

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-272-59

Query Match 100.0%; Score 41; DB 4; Length 874;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 126 NAPVSIPQ 133

RESULT 37

US-10-623-272-1

; Sequence 1, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H3' human activity dependent neurotrophic factor
; OTHER INFORMATION: III (ADNF III) clone
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (801)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (817)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (821)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:


```

; NAME/KEY: MOD_RES
; LOCATION: (833)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (854)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (866)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (870)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (877)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (882)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (922)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (948)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (959)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (964)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (967)
; OTHER INFORMATION: Xaa = unknown
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (980)
; OTHER INFORMATION: Xaa = unknown
US-10-623-272-1

```

```

Query Match          100.0%; Score 41; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 65;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 NAPVSIPQ 8
        |||||
Db      52 NAPVSIPQ 59

```

RESULT 38

US-09-364-609-8

```
; Sequence 8, Application US/09364609
; Publication No. US20030036521A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brenneman, Douglas E.
; APPLICANT: Zamostiano, Rachel
; APPLICANT: Gelber, Edgar
; APPLICANT: Pinhasov, Albert
; APPLICANT: Bassan, Merav
; APPLICANT: Ramot University Authority for Applied Research &
; APPLICANT: Industrial Development, Ltd.
; TITLE OF INVENTION: Methods of Inhibiting Cancer Cells With ADNF III
; TITLE OF INVENTION: Antisense Oligonucleotides
; FILE REFERENCE: 019856-000100US
; CURRENT APPLICATION NUMBER: US/09/364,609
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1102
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human activity dependent neurotrophic factor III
;   OTHER INFORMATION: (ADNF III) cDNA
```

US-09-364-609-8

```
Query Match          100.0%; Score 41; DB 3; Length 1102;
Best Local Similarity 100.0%; Pred. No. 72;
Matches      8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
Qy      1 NAPVSIPQ 8
        |||||
Db      354 NAPVSIPQ 361
```

RESULT 39

US-10-164-432-2

```
; Sequence 2, Application US/10164432
; Publication No. US20030166544A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Inc.
; APPLICANT: Clark, Abbot F.
; APPLICANT: Debra, Shade L.
; TITLE OF INVENTION: The Use of ADNP for the Treatment of Glaucomatous Optic
Neuropathy
; FILE REFERENCE: 1975A US
; CURRENT APPLICATION NUMBER: US/10/164,432
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/921,029
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/230,964
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-164-432-2

Query Match 100.0%; Score 41; DB 4; Length 1102;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 354 NAPVSIPQ 361

RESULT 40

US-10-221-625-49
; Sequence 49, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221,625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 1929822CD1
US-10-221-625-49

Query Match 100.0%; Score 41; DB 4; Length 1102;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 354 NAPVSIPQ 361

RESULT 41

US-10-623-272-28

; Sequence 28, Application US/10623272
 ; Publication No. US20040053313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gozes, Illana
 ; APPLICANT: Brenneman, Douglas E.
 ; APPLICANT: Bassan, Merav
 ; APPLICANT: Zamostiano, Rachel
 ; APPLICANT: The Government of the United States of America
 ; APPLICANT: as represented by the Secretary of the
 ; APPLICANT: Department of Health and Human Services
 ; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
 ; FILE REFERENCE: 015280-291200US
 ; CURRENT APPLICATION NUMBER: US/10/623,272
 ; CURRENT FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 28
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:sequence of p25
 ; OTHER INFORMATION: clone with structural similarity to active peptide
 ; OTHER INFORMATION: of ADNF I

US-10-623-272-28

Query Match 87.8%; Score 36; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 |||||
 Db 3 NAPVSIP 9

RESULT 42

US-10-169-048-18

; Sequence 18, Application US/10169048
 ; Publication No. US20030072769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Clarke, Edna Elizabeth
 ; APPLICANT: Zhou, Liqing
 ; APPLICANT: Shea, Jacqueline Elizabeth
 ; APPLICANT: Feldman, Robert Graham
 ; APPLICANT: Holden, David William
 ; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And
 Their Use

; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-18

Query Match 87.8%; Score 36; DB 4; Length 510;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | | |
Db 215 NTPISIPQ 222

RESULT 43

US-10-264-213-145

; Sequence 145, Application US/10264213
; Publication No. US20040009490A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Lubbers, Mark William
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them, and methods for using them.
; FILE REFERENCE: 11000.1043c3
; CURRENT APPLICATION NUMBER: US/10/264,213
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-145

Query Match 87.8%; Score 36; DB 4; Length 510;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | | |
Db 215 NTPISIPQ 222

RESULT 44

US-10-282-122A-42533

; Sequence 42533, Application US/10282122A
; Publication No. US20040029129A1

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42533
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-42533

```

```

Query Match          87.8%; Score 36; DB 4; Length 510;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches      6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy          1 NAPVSIPQ 8
             | :|||
Db          215 NTPISIPQ 222

```

```

RESULT 45
US-10-282-122A-74577

```

```

; Sequence 74577, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74577
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74577

```

```

Query Match          87.8%; Score 36; DB 4; Length 510;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches      6; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPO 8
        | | : | | |
Db      215 NTPISIPQ 222

```

RESULT 46

US-11-144-352-18

```
; Sequence 18, Application US/11144352
; Publication No. US20050232942A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And
Their Use
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/11/144,352
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US/10/169,048
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-11-144-352-18
```

```
Query Match          87.8%; Score 36; DB 6; Length 510;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches      6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 NAPVSIPQ 8
        | | : | | |
Db      215 NTPISIPQ 222
```

RESULT 47

US-10-282-122A-72068

```
; Sequence 72068, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
```



```

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72068
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Streptococcus mutans
US-10-282-122A-72068

```

```

Query Match          87.8%; Score 36; DB 4; Length 511;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches      6; Conservative    1; Mismatches    1; Indels      0; Gaps      0;

```

```

Qy      1 NAPVSIPQ 8
        | | : | | |
Db      215 NTPISIPQ 222

```

RESULT 48

```

US-10-425-114-58854
; Sequence 58854, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58854

```

; LENGTH: 321
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701164854_FLI.pep
US-10-425-114-58854

Query Match 85.4%; Score 35; DB 4; Length 321;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
|||:|
Db 21 NAPVSP 27

RESULT 49

US-11-097-143-39252
; Sequence 39252, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39252
; LENGTH: 331
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-39252

Query Match 85.4%; Score 35; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
| | | | |
Db 31 APVSIPQ 37

RESULT 50

US-10-655-799-38

; Sequence 38, Application US/10655799
; Publication No. US20040126843A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriss, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074U
; CURRENT APPLICATION NUMBER: US/10/655,799
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-655-799-38

Query Match 85.4%; Score 35; DB 4; Length 808;
Best Local Similarity 75.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| : | | : | | |
Db 271 NSPVAIPQ 278

Search completed: April 26, 2006, 00:26:39
Job time : 179 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 00:14:52 ; Search time 223 Seconds
 (without alignments)
 25.310 Million cell updates/sec

Title: US-10-748-765-2
 Perfect score: 41
 Sequence: 1 NAPVSIPQ 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	41	100.0	823	1	ADNP_RAT	Q9jkl8	rattus norv
2	41	100.0	828	1	ADNP_MOUSE	Q9z103	mus musculu
3	41	100.0	922	2	Q5RKY4_MOUSE	Q5rky4	mus musculu
4	41	100.0	1004	2	Q5BL11_MOUSE	Q5bl11	mus musculu
5	41	100.0	1089	2	Q6ZQ47_MOUSE	Q6zq47	mus musculu
6	41	100.0	1102	1	ADNP_HUMAN	Q9h2p0	homo sapien
7	41	100.0	1102	2	Q5BKU2_HUMAN	Q5bku2	homo sapien
8	41	100.0	1102	2	Q6DHZ8_HUMAN	Q6dhz8	homo sapien
9	36	87.8	445	2	Q6C9B5_YARLI	Q6c9b5	yarrowia li
10	36	87.8	470	2	Q82YW3_ENTFA	Q82yw3	enterococcu
11	36	87.8	481	2	Q8E338_STRA3	Q8e338	streptococc
12	36	87.8	510	2	Q5XC32_STRP6	Q5xc32	streptococc
13	36	87.8	510	2	Q99ZK7_STRPY	Q99zk7	streptococc
14	36	87.8	510	2	Q8P0Z3_STRP8	Q8p0z3	streptococc
15	36	87.8	510	2	Q8K7F1_STRP3	Q8k7f1	streptococc

16	36	87.8	511	2	Q8DUC1_STRMU	Q8duc1 streptococc
17	36	87.8	631	2	Q9I2G3_PSEAE	Q9i2g3 pseudomonas
18	36	87.8	707	2	Q4M171_9BURK	Q4m171 burkholderi
19	36	87.8	1396	2	Q6KAS0_MOUSE	Q6kas0 mus musculu
20	36	87.8	1502	1	GEMI5_MOUSE	Q8bx17 mus musculu
21	35	85.4	189	2	Q8SZD3_DROME	Q8szd3 drosophila
22	35	85.4	189	2	Q9V7Z8_DROME	Q9v7z8 drosophila
23	35	85.4	299	2	Q92XP0_RHIME	Q92xp0 rhizobium m
24	35	85.4	389	2	Q4K637_PSEF5	Q4k637 pseudomonas
25	35	85.4	3415	2	Q9XCF3_MYCAV	Q9xcf3 mycobacteri
26	35	85.4	4027	2	Q740V0_MYCPA	Q740v0 mycobacteri
27	34	82.9	136	2	Q28744_ARCFU	Q28744 archaeoglob
28	34	82.9	158	2	Q8BQB7_MOUSE	Q8bqb7 mus musculu
29	34	82.9	458	2	Q5NIK3_FRATT	Q5nik3 francisella
30	34	82.9	464	2	Q6FFK0_ACIAD	Q6ffk0 acinetobact
31	34	82.9	503	2	Q84LK3_ORYSA	Q84lk3 oryza sativ
32	34	82.9	505	2	Q9V3B2_DROME	Q9v3b2 drosophila
33	34	82.9	597	2	Q6MAF9_PARUW	Q6maf9 parachlamyd
34	34	82.9	685	2	Q50YT9_ENTHI	Q50yt9 entamoeba h
35	34	82.9	946	2	Q4R3H9_MACFA	Q4r3h9 macaca fasc
36	34	82.9	1272	1	AFF2_MOUSE	O55112 mus musculu
37	34	82.9	1272	1	AFF2_PANTR	Q7yqm2 pan troglod
38	34	82.9	1272	1	AFF2_PONPY	Q7yqm1 pongo pygma
39	34	82.9	1272	2	Q7Z400_HUMAN	Q7z400 homo sapien
40	34	82.9	1311	1	AFF2_HUMAN	P51816 homo sapien
41	34	82.9	1789	2	Q8T145_DICDI	Q8t145 dictyosteli
42	33	80.5	104	2	Q8A044_BACTN	Q8a044 bacteroides
43	33	80.5	129	2	Q5CXV6_CRYPV	Q5cxv6 cryptospori
44	33	80.5	129	2	Q5CLN5_CRYHO	Q5cln5 cryptospori
45	33	80.5	159	2	Q57QN6_SALCH	Q57qn6 salmonella
46	33	80.5	197	1	WRBA_SALPA	Q5pg91 salmonella
47	33	80.5	197	1	WRBA_SALTI	Q8z7n9 salmonella
48	33	80.5	197	1	WRBA_SALTY	Q8zq40 salmonella
49	33	80.5	231	1	HIS2_HELHP	Q7vj02 helicobacte
50	33	80.5	253	2	Q6W4C2_DROME	Q6w4c2 drosophila
51	33	80.5	253	2	Q6W4C3_DROME	Q6w4c3 drosophila
52	33	80.5	253	2	Q6W4E3_DROME	Q6w4e3 drosophila
53	33	80.5	258	2	Q6C7G0_YARLI	Q6c7g0 yarrowia li
54	33	80.5	289	2	Q56IC4_OSTNU	Q56ic4 ostrinia nu
55	33	80.5	290	2	Q56IC3_OSTNU	Q56ic3 ostrinia nu
56	33	80.5	290	2	Q56IC2_OSTNU	Q56ic2 ostrinia nu
57	33	80.5	350	2	Q6FEX1_ACIAD	Q6fex1 acinetobact
58	33	80.5	467	1	EUTA_SALTY	Q9zfv2 salmonella
59	33	80.5	467	2	Q8Z4U1_SALTI	Q8z4u1 salmonella
60	33	80.5	468	2	Q6LW58_PHOPR	Q6lw58 photobacter
61	33	80.5	479	2	Q5IRM9_ARATH	Q5irm9 arabidopsis
62	33	80.5	505	2	Q5IRX4_ARATH	Q5irx4 arabidopsis
63	33	80.5	520	2	Q7XU21_ORYSA	Q7xu21 oryza sativ
64	33	80.5	555	2	Q5ZLA1_CHICK	Q5zla1 gallus gall
65	33	80.5	556	2	Q4NIX3_9MICC	Q4nix3 arthrobacte
66	33	80.5	557	2	Q6TPF1_CAEEL	Q6tpf1 caenorhabdi
67	33	80.5	574	1	NEUL1_HUMAN	O76050 homo sapien
68	33	80.5	574	1	NEURL_MOUSE	Q923s6 mus musculu
69	33	80.5	623	1	ARFM_ARATH	Q9fx25 arabidopsis
70	33	80.5	639	2	Q5GZ00_XANOR	Q5gz00 xanthomonas
71	33	80.5	674	1	CIN_DROME	P39205 drosophila
72	33	80.5	706	2	Q4Q1B3_LEIMA	Q4qlb3 leishmania

73	33	80.5	776	2	Q4WK55_ASPFU	Q4wk55	aspergillus
74	33	80.5	792	2	Q6TPF8_CAEEL	Q6tpf8	caenorhabdi
75	33	80.5	825	2	Q4SGA4_TETNG	Q4sga4	tetraodon n
76	33	80.5	836	2	Q5B254_EMENI	Q5b254	aspergillus
77	33	80.5	926	2	Q6TPF2_CAEEL	Q6tpf2	caenorhabdi
78	33	80.5	1027	2	Q4P181_USTMA	Q4p181	ustilago ma
79	33	80.5	1130	2	Q9P3N5_NEUCR	Q9p3n5	neurospora
80	33	80.5	1183	2	Q7SH03_NEUCR	Q7sh03	neurospora
81	33	80.5	1268	2	Q4I1A9_GIBZE	Q4ila9	gibberella
82	33	80.5	1351	1	OVO_DROME	P51521	drosophila
83	33	80.5	1509	2	Q7JM47_CAEEL	Q7jm47	caenorhabdi
84	33	80.5	1692	2	Q7JM48_CAEEL	Q7jm48	caenorhabdi
85	33	80.5	1888	2	Q7JM45_CAEEL	Q7jm45	caenorhabdi
86	33	80.5	1927	2	Q7JM46_CAEEL	Q7jm46	caenorhabdi
87	33	80.5	2048	2	Q7JM42_CAEEL	Q7jm42	caenorhabdi
88	33	80.5	2066	2	Q22190_CAEEL	Q22190	caenorhabdi
89	33	80.5	2101	2	Q7JM43_CAEEL	Q7jm43	caenorhabdi
90	33	80.5	2134	2	Q7JM44_CAEEL	Q7jm44	caenorhabdi
91	33	80.5	3243	2	Q4HB00_9DEIO	Q4hb00	deinococcus
92	32	78.0	93	2	Q94228_CAEEL	Q94228	caenorhabdi
93	32	78.0	107	2	Q61T34_CAEER	Q61t34	caenorhabdi
94	32	78.0	144	2	Q6WQJ4_STRPY	Q6wqj4	streptococc
95	32	78.0	145	2	Q6H0M8_STRPY	Q6h0m8	streptococc
96	32	78.0	145	2	Q6H0M9_STRPY	Q6h0m9	streptococc
97	32	78.0	145	2	Q6H0N1_STRPY	Q6h0n1	streptococc
98	32	78.0	145	2	Q6WQJ3_STRPY	Q6wqj3	streptococc
99	32	78.0	145	2	Q6WQJ6_STRPY	Q6wqj6	streptococc
100	32	78.0	145	2	Q6WQJ7_STRPY	Q6wqj7	streptococc
101	32	78.0	145	2	Q6WQJ8_STRPY	Q6wqj8	streptococc
102	32	78.0	145	2	Q6WQK0_STRPY	Q6wqk0	streptococc
103	32	78.0	145	2	Q6WQK1_STRPY	Q6wqk1	streptococc
104	32	78.0	145	2	Q933L4_STREQ	Q933l4	streptococc
105	32	78.0	145	2	Q93PG6_STREQ	Q93pg6	streptococc
106	32	78.0	145	2	Q93PG7_STREQ	Q93pg7	streptococc
107	32	78.0	145	2	Q93PG8_STREQ	Q93pg8	streptococc
108	32	78.0	145	2	Q9ETP6_STRPY	Q9etp6	streptococc
109	32	78.0	145	2	Q9ETW9_STRPY	Q9etw9	streptococc
110	32	78.0	145	2	Q9EW28_STRPY	Q9ew28	streptococc
111	32	78.0	145	2	Q9EW29_STRPY	Q9ew29	streptococc
112	32	78.0	145	2	Q9EW30_STRPY	Q9ew30	streptococc
113	32	78.0	145	2	Q9EW31_STRPY	Q9ew31	streptococc
114	32	78.0	145	2	Q9EW32_STRPY	Q9ew32	streptococc
115	32	78.0	145	2	Q9EW33_STRPY	Q9ew33	streptococc
116	32	78.0	145	2	Q9EW34_STRPY	Q9ew34	streptococc
117	32	78.0	145	2	Q9EW35_STRPY	Q9ew35	streptococc
118	32	78.0	145	2	Q9EW36_STRPY	Q9ew36	streptococc
119	32	78.0	145	2	Q9EW37_STRPY	Q9ew37	streptococc
120	32	78.0	145	2	Q9EW38_STRPY	Q9ew38	streptococc
121	32	78.0	145	2	Q9EW39_STRPY	Q9ew39	streptococc
122	32	78.0	153	2	Q4U9K3_THEAN	Q4u9k3	theileria a
123	32	78.0	154	2	Q9DUH3_HPBVO	Q9duh3	hepatitis b
124	32	78.0	154	2	Q9DUH7_HPBVO	Q9duh7	hepatitis b
125	32	78.0	154	2	Q9YJS9_HPBVO	Q9yjs9	hepatitis b
126	32	78.0	191	2	Q9QCX2_9VIRU	Q9qcx2	chayote mos
127	32	78.0	202	2	Q7W008_BORPE	Q7w008	bordetella
128	32	78.0	202	2	Q7W3K3_BORPA	Q7w3k3	bordetella
129	32	78.0	202	2	Q7WEX8_BORBR	Q7wex8	bordetella

130	32	78.0	248	2	Q5TS04_ANOGA	Q5ts04 anopheles g
131	32	78.0	249	2	Q8YY75_ANASP	Q8yy75 anabaena sp
132	32	78.0	301	2	Q8ZF00_YERPE	Q8zf00 yersinia pe
133	32	78.0	301	2	Q66AZ2_YERPS	Q66az2 yersinia ps
134	32	78.0	312	2	Q8L2G9_ERWCH	Q8l2g9 erwinia chr
135	32	78.0	344	2	Q6VMW1_MENPI	Q6vmw1 mentha pipe
136	32	78.0	344	2	Q6VMW2_MENPI	Q6vmw2 mentha pipe
137	32	78.0	359	2	Q7YQQ5_LOXAF	Q7yqq5 loxodonta a
138	32	78.0	361	2	Q7YQQ4_ELEMA	Q7yqq4 elephas max
139	32	78.0	391	2	Q4N107_THEPA	Q4n107 theileria p
140	32	78.0	394	2	Q5XE62_STRP6	Q5xe62 streptococc
141	32	78.0	394	2	Q9A1R4_STRPY	Q9a1r4 streptococc
142	32	78.0	394	2	Q8P2V3_STRP8	Q8p2v3 streptococc
143	32	78.0	394	2	Q8K8T7_STRP3	Q8k8t7 streptococc
144	32	78.0	399	2	Q5V5K5_HALMA	Q5v5k5 haloarcula
145	32	78.0	400	2	Q9XD81_9ACTO	Q9xd81 streptomyce
146	32	78.0	412	2	Q8DJU4_SYNEL	Q8dju4 synechococc
147	32	78.0	460	2	Q7VDH5_PROMA	Q7vdh5 prochloroco
148	32	78.0	467	2	Q4P8B1_USTMA	Q4p8b1 ustilago ma
149	32	78.0	468	2	Q9ZUR7_ARATH	Q9zur7 arabidopsis
150	32	78.0	470	2	Q4RVE1_TETNG	Q4rve1 tetraodon n
151	32	78.0	502	2	Q6BD88_9POAL	Q6bd88 zoysia tenu
152	32	78.0	503	2	Q6BDA3_9POAL	Q6bda3 zoysia tenu
153	32	78.0	504	2	Q6BD90_9POAL	Q6bd90 zoysia tenu
154	32	78.0	504	2	Q6BD99_9POAL	Q6bd99 zoysia tenu
155	32	78.0	508	2	Q4QH41_LEIMA	Q4qh41 leishmania
156	32	78.0	555	2	Q8UVQ6_XENLA	Q8uvq6 xenopus lae
157	32	78.0	555	2	Q6GQD2_XENLA	Q6gqd2 xenopus lae
158	32	78.0	572	1	PUT2_EMENI	Q9p8i0 emericella
159	32	78.0	572	2	Q5BCJ7_EMENI	Q5bcj7 aspergillus
160	32	78.0	617	2	Q4K8E1_PSEF5	Q4k8e1 pseudomonas
161	32	78.0	640	2	Q5TNL6_ANOGA	Q5tnl6 anopheles g
162	32	78.0	657	2	Q7CY07_AGRT5	Q7cy07 agrobacteri
163	32	78.0	662	2	Q8IR58_DROME	Q8ir58 drosophila
164	32	78.0	668	2	Q8UDT1_AGRT5	Q8udt1 agrobacteri
165	32	78.0	692	2	Q517P5_ENTHI	Q517p5 entamoeba h
166	32	78.0	710	2	Q4V837_XENLA	Q4v837 xenopus lae
167	32	78.0	711	2	Q6GPU3_XENLA	Q6gpu3 xenopus lae
168	32	78.0	713	2	Q6P1W0_XENTR	Q6plw0 xenopus tro
169	32	78.0	747	2	Q7S464_NEUCR	Q7s464 neurospora
170	32	78.0	747	2	Q4REZ0_TETNG	Q4rez0 tetraodon n
171	32	78.0	923	2	Q4FWG0_LEIMA	Q4fwg0 leishmania
172	32	78.0	943	2	Q9KZN0_STRCO	Q9kzn0 streptomyce
173	32	78.0	1017	2	Q7VEU8_MYCBO	Q7veu8 mycobacteri
174	32	78.0	1017	2	O06586_MYCTU	O06586 mycobacteri
175	32	78.0	1125	2	Q86IF5_DICDI	Q86if5 dictyosteli
176	32	78.0	1164	2	Q559A0_DICDI	Q559a0 dictyosteli
177	32	78.0	1357	2	Q6BMU2_DEBHA	Q6bmu2 debaryomyce
178	32	78.0	1368	2	Q7MLW3_VIBVY	Q7mlw3 vibrio vuln
179	32	78.0	1414	2	Q63330_RAT	Q63330 rattus norv
180	32	78.0	1498	2	Q96VK6_EMENI	Q96vk6 emericella
181	32	78.0	2774	1	MAP1A_RAT	P34926 rattus norv
182	32	78.0	7480	2	Q4IP09_GIBZE	Q4ip09 gibberella
183	31	75.6	102	2	Q4FVL8_9GAMM	Q4fvl8 psychrobact
184	31	75.6	121	2	Q6ZT42_HUMAN	Q6zt42 homo sapien
185	31	75.6	132	2	Q913H4_9ADEN	Q913h4 human adeno
186	31	75.6	135	2	Q912I9_9ADEN	Q912i9 human adeno

187	31	75.6	137	2	Q647K5_9ARCH	Q647k5 uncultured
188	31	75.6	151	2	Q9LV64_ARATH	Q9lv64 arabidopsis
189	31	75.6	155	2	Q6TFR9_ERWAM	Q6tfr9 erwinia amy
190	31	75.6	157	2	Q7UXZ8_RHOBA	Q7uxz8 rhodopirell
191	31	75.6	159	1	Y822_CHLMU	Q9pjk7 chlamydia m
192	31	75.6	167	2	Q8LEL0_ARATH	Q8lel0 arabidopsis
193	31	75.6	179	2	Q5B4A1_EMENI	Q5b4a1 aspergillus
194	31	75.6	181	2	Q5YMW5_NOCFA	Q5ymw5 nocardia fa
195	31	75.6	194	2	Q829A2_STRAW	Q829a2 streptomyce
196	31	75.6	203	2	Q8XR70_RALSO	Q8xr70 ralstonia s
197	31	75.6	232	2	Q51QZ6_MAGGR	Q51qz6 magnaporthe
198	31	75.6	243	1	YK1E_SCHPO	Q9hdx6 schizosacch
199	31	75.6	246	2	Q66KN6_XENLA	Q66kn6 xenopus lae
200	31	75.6	246	2	Q6INB3_XENLA	Q6inb3 xenopus lae
201	31	75.6	250	1	RNH2_LACAC	Q5fke4 lactobacill
202	31	75.6	250	1	RNH2_LACJO	Q74jk1 lactobacill
203	31	75.6	260	2	Q4X0K9_ASPFU	Q4x0k9 aspergillus
204	31	75.6	263	1	RNH2_BACHD	Q9z9s0 bacillus ha
205	31	75.6	266	2	Q5YPL3_NOCFA	Q5ypl3 nocardia fa
206	31	75.6	269	2	Q582X9_9TRYP	Q582x9 trypanosoma
207	31	75.6	282	2	Q99CY7_BHV4	Q99cy7 bovine herp
208	31	75.6	287	2	Q8GDL3_PHOLU	Q8gdl3 photorhabdu
209	31	75.6	296	2	O90768_9ADEN	O90768 human adeno
210	31	75.6	297	2	Q7ZWY7_XENLA	Q7zwy7 xenopus lae
211	31	75.6	299	2	O90765_ADE09	O90765 human adeno
212	31	75.6	300	2	Q4IIY0_GIBZE	Q4iiy0 gibberella
213	31	75.6	305	2	Q5H8B7_9ADEN	Q5h8b7 human adeno
214	31	75.6	305	2	Q5H8B8_9ADEN	Q5h8b8 human adeno
215	31	75.6	305	2	Q60HI4_9ADEN	Q60hi4 human adeno
216	31	75.6	305	2	Q6BEA9_ADE04	Q6bea9 human adeno
217	31	75.6	305	2	Q6BEB0_ADE04	Q6beb0 human adeno
218	31	75.6	305	2	Q6BEB1_ADE04	Q6beb1 human adeno
219	31	75.6	305	2	Q6BEB2_ADE04	Q6beb2 human adeno
220	31	75.6	305	2	Q6BEB3_ADE04	Q6beb3 human adeno
221	31	75.6	305	2	Q76I31_9ADEN	Q76i31 human adeno
222	31	75.6	305	2	Q76I32_9ADEN	Q76i32 human adeno
223	31	75.6	305	2	Q76I33_9ADEN	Q76i33 human adeno
224	31	75.6	305	2	Q76I34_9ADEN	Q76i34 human adeno
225	31	75.6	305	2	Q76I35_9ADEN	Q76i35 human adeno
226	31	75.6	305	2	Q76I36_ADE08	Q76i36 human adeno
227	31	75.6	305	2	Q76I37_ADE08	Q76i37 human adeno
228	31	75.6	305	2	Q76I38_ADE08	Q76i38 human adeno
229	31	75.6	305	2	Q76I39_ADE04	Q76i39 human adeno
230	31	75.6	305	2	Q76I40_9ADEN	Q76i40 human adeno
231	31	75.6	305	2	Q76I41_9ADEN	Q76i41 human adeno
232	31	75.6	305	2	Q76I42_9ADEN	Q76i42 human adeno
233	31	75.6	305	2	Q76I43_9ADEN	Q76i43 human adeno
234	31	75.6	305	2	Q76I44_9ADEN	Q76i44 human adeno
235	31	75.6	305	2	Q76I45_9ADEN	Q76i45 human adeno
236	31	75.6	305	2	Q76I46_9ADEN	Q76i46 human adeno
237	31	75.6	305	2	Q76I47_9ADEN	Q76i47 human adeno
238	31	75.6	305	2	Q76I48_9ADEN	Q76i48 human adeno
239	31	75.6	305	2	Q76I49_9ADEN	Q76i49 human adeno
240	31	75.6	305	2	Q76I50_9ADEN	Q76i50 human adeno
241	31	75.6	305	2	Q76I51_9ADEN	Q76i51 human adeno
242	31	75.6	305	2	Q76I52_9ADEN	Q76i52 human adeno
243	31	75.6	305	2	Q76I53_9ADEN	Q76i53 human adeno

244	31	75.6	305	2	Q76I54_9ADEN	Q76i54 human adeno
245	31	75.6	305	2	Q76I55_9ADEN	Q76i55 human adeno
246	31	75.6	305	2	Q76I56_9ADEN	Q76i56 human adeno
247	31	75.6	305	2	Q76I57_9ADEN	Q76i57 human adeno
248	31	75.6	305	2	Q76I58_9ADEN	Q76i58 human adeno
249	31	75.6	305	2	Q76I59_9ADEN	Q76i59 human adeno
250	31	75.6	305	2	Q76I60_9ADEN	Q76i60 human adeno
251	31	75.6	305	2	Q76I61_9ADEN	Q76i61 human adeno
252	31	75.6	305	2	Q76I62_9ADEN	Q76i62 human adeno
253	31	75.6	305	2	Q76I63_9ADEN	Q76i63 human adeno
254	31	75.6	305	2	Q76I64_9ADEN	Q76i64 human adeno
255	31	75.6	305	2	Q76I65_9ADEN	Q76i65 human adeno
256	31	75.6	305	2	Q76I66_ADE17	Q76i66 human adeno
257	31	75.6	305	2	Q76I67_ADE15	Q76i67 human adeno
258	31	75.6	305	2	Q76I68_9ADEN	Q76i68 human adeno
259	31	75.6	305	2	Q76I69_9ADEN	Q76i69 human adeno
260	31	75.6	305	2	Q76I70_ADE09	Q76i70 human adeno
261	31	75.6	305	2	Q76I71_ADE08	Q76i71 human adeno
262	31	75.6	306	2	Q566X9_BRARE	Q566x9 brachydanio
263	31	75.6	310	2	O90769_9ADEN	O90769 human adeno
264	31	75.6	311	2	Q7QLQ4_ANOGA	Q7qlq4 anopheles g
265	31	75.6	312	2	O90762_ADE01	O90762 human adeno
266	31	75.6	312	2	O90763_ADE06	O90763 human adeno
267	31	75.6	312	2	O90770_9ADEN	O90770 human adeno
268	31	75.6	314	2	Q6CQ55_KLULA	Q6cq55 kluyveromyc
269	31	75.6	314	2	Q810T0_MOUSE	Q810t0 mus musculu
270	31	75.6	317	2	Q4FX12_LEIMA	Q4fx12 leishmania
271	31	75.6	320	2	Q63L68_BURPS	Q63l68 burkholderi
272	31	75.6	323	1	FMT_PORGI	Q7mte3 porphyromon
273	31	75.6	323	2	Q5B3E9_EMENI	Q5b3e9 aspergillus
274	31	75.6	325	2	O90766_ADE17	O90766 human adeno
275	31	75.6	333	2	Q5V3K7_HALMA	Q5v3k7 haloarcula
276	31	75.6	333	2	Q8KGB6_CHLTE	Q8kgb6 chlorobium
277	31	75.6	341	2	Q9XAM1_STRCO	Q9xam1 streptomyce
278	31	75.6	344	2	Q8G4A8_BIFLO	Q8g4a8 bifidobacte
279	31	75.6	350	1	YCEA_SALTI	Q8z7l5 salmonella
280	31	75.6	350	1	YCEA_SALTY	Q8zq23 salmonella
281	31	75.6	350	2	Q57QK2_SALCH	Q57qk2 salmonella
282	31	75.6	350	2	Q5PGX0_SALPA	Q5pgx0 salmonella
283	31	75.6	354	2	Q8EHQ1_SHEON	Q8ehq1 shewanella
284	31	75.6	358	2	Q5F6R5_NEIG1	Q5f6r5 neisseria g
285	31	75.6	358	2	Q9JT27_NEIMA	Q9jt27 neisseria m
286	31	75.6	358	2	Q9K0U1_NEIMB	Q9k0u1 neisseria m
287	31	75.6	380	2	Q6CA36_YARLI	Q6ca36 yarrowia li
288	31	75.6	382	2	Q8RBH1_THETN	Q8rbh1 thermoanaer
289	31	75.6	390	2	Q5YRP3_NOCFA	Q5yrp3 nocardia fa
290	31	75.6	392	2	Q9ZGI9_9BURK	Q9zgi9 alcaligenes
291	31	75.6	392	2	Q6UFW3_9PSED	Q6ufw3 pseudomonas
292	31	75.6	393	1	THIL_MYCLE	P46707 mycobacteri
293	31	75.6	393	2	O87111_COMAC	O87111 comamonas a
294	31	75.6	393	2	Q4LM20_9BURK	Q4lm20 burkholderi
295	31	75.6	393	2	Q4LPE9_9BURK	Q4lpe9 burkholderi
296	31	75.6	393	2	Q6GCB8_STAAS	Q6gcb8 staphylococ
297	31	75.6	393	2	Q6GJW4_STAAR	Q6gjw4 staphylococ
298	31	75.6	393	2	Q7A7L2_STAAN	Q7a7l2 staphylococ
299	31	75.6	393	2	Q8NY95_STAAN	Q8ny95 staphylococ
300	31	75.6	393	2	Q99WM3_STAAM	Q99wm3 staphylococ

301	31	75.6	393	2	Q5HIU0_STAAC	Q5hiu0	staphylococ
302	31	75.6	394	1	THIL_THIVI	P45363	thiocystis
303	31	75.6	395	2	Q8UIP6_AGRT5	Q8uip6	agrobacteri
304	31	75.6	405	2	Q6A8E8_PROAC	Q6a8e8	propionibac
305	31	75.6	407	2	Q9VEL7_DROME	Q9vel7	drosophila
306	31	75.6	420	2	Q6AZA0_BRARE	Q6aza0	brachydanio
307	31	75.6	424	2	Q43828_SORBI	Q43828	sorghum bic
308	31	75.6	424	2	Q82XZ0_NITEU	Q82xz0	nitrosomona
309	31	75.6	431	2	Q8VTH5_9PAST	Q8vth5	pasteurella
310	31	75.6	433	2	Q4NC47_9MICC	Q4nc47	arthrobacte
311	31	75.6	434	2	Q7TML8_MOUSE	Q7tml8	mus musculu
312	31	75.6	440	2	Q61SW9_CAEBR	Q61sw9	caenorhabdi
313	31	75.6	456	2	Q8C9W4_MOUSE	Q8c9w4	mus musculu
314	31	75.6	459	1	IL7RA_MOUSE	P16872	mus musculu
315	31	75.6	459	2	Q9R0C1_MOUSE	Q9r0c1	mus musculu
316	31	75.6	460	2	Q4J888_SULAC	Q4j888	sulfolobus
317	31	75.6	468	2	Q82Y63_NITEU	Q82y63	nitrosomona
318	31	75.6	472	2	Q67TB7_SYMTH	Q67tb7	symbiobacte
319	31	75.6	481	2	Q8TWG6_METKA	Q8twg6	methanopyru
320	31	75.6	482	2	Q8DIA6_SYNEL	Q8dia6	synechococc
321	31	75.6	490	2	Q8PJJ4_XANAC	Q8pjj4	xanthomonas
322	31	75.6	497	2	Q6D8B4_ERWCT	Q6d8b4	erwinia car
323	31	75.6	505	2	Q53CF4_MAIZE	Q53cf4	zea mays (m
324	31	75.6	518	2	Q57X10_9TRYP	Q57x10	trypanosoma
325	31	75.6	518	2	Q6GA43_STAAS	Q6ga43	staphylococ
326	31	75.6	518	2	Q6GHR5_STAAR	Q6ghr5	staphylococ
327	31	75.6	518	2	Q5HGR1_STAAC	Q5hgr1	staphylococ
328	31	75.6	518	2	Q7A626_STAAN	Q7a626	staphylococ
329	31	75.6	518	2	Q8NX43_STAAW	Q8nx43	staphylococ
330	31	75.6	518	2	Q99UT9_STAAM	Q99ut9	staphylococ
331	31	75.6	521	2	Q5HKJ2_STA EQ	Q5hkj2	staphylococ
332	31	75.6	521	2	Q8CTX2_STAEP	Q8ctx2	staphylococ
333	31	75.6	525	2	Q918H3_9BETA	Q918h3	baboon cyto
334	31	75.6	536	2	Q6CDT6_YARLI	Q6cdt6	yarrowia li
335	31	75.6	536	2	Q72BV4_DESVH	Q72bv4	desulfovibr
336	31	75.6	537	2	Q73TW1_MYCPA	Q73tw1	mycobacteri
337	31	75.6	539	2	Q5GY42_XANOR	Q5gy42	xanthomonas
338	31	75.6	556	2	Q63HN1_HUMAN	Q63hn1	homo sapien
339	31	75.6	556	2	Q6ZRJ7_HUMAN	Q6zrj7	homo sapien
340	31	75.6	556	2	Q8EP38_OCEIH	Q8ep38	oceanobacil
341	31	75.6	557	1	PAC1_PSES3	P15557	pseudomonas
342	31	75.6	557	1	PAC1_PSESV	Q05053	pseudomonas
343	31	75.6	561	2	Q5QHQ6_LEIMA	Q5qhq6	leishmania
344	31	75.6	576	2	Q9K5E3_CORGL	Q9k5e3	corynebacte
345	31	75.6	580	2	Q8Y2A4_RALSO	Q8y2a4	ralstonia s
346	31	75.6	593	2	Q7MC46_VIBVY	Q7mc46	vibrio vuln
347	31	75.6	624	2	Q52EB7_MAGGR	Q52eb7	magnaporthe
348	31	75.6	636	2	Q4WZQ3_ASPFU	Q4wzq3	aspergillus
349	31	75.6	666	2	Q89YD3_BRAJA	Q89yd3	bradyrhizob
350	31	75.6	672	2	Q9W7B7_BRARE	Q9w7b7	brachydanio
351	31	75.6	679	2	O94033_CANAL	O94033	candida alb
352	31	75.6	679	2	Q5AI80_CANAL	Q5ai80	candida alb
353	31	75.6	685	2	Q8FT49_COREF	Q8ft49	corynebacte
354	31	75.6	687	2	Q9IAL0_BRARE	Q9ial0	brachydanio
355	31	75.6	687	2	Q7ZTU9_BRARE	Q7ztu9	brachydanio
356	31	75.6	688	2	Q8NQ45_CORGL	Q8nq45	corynebacte
357	31	75.6	700	2	Q8N0R5_BOMMO	Q8n0r5	bombyx mori

358	31	75.6	715	2	Q4PA05_USTMA	Q4pa05	ustilago ma
359	31	75.6	764	2	Q6N7G6_RHOPA	Q6n7g6	rhodopseudo
360	31	75.6	772	2	Q6NYK4_BRARE	Q6nyk4	brachydanio
361	31	75.6	776	2	Q6PNC5_BRARE	Q6pnc5	brachydanio
362	31	75.6	787	1	OBP_HHV7J	P52379	human herpe
363	31	75.6	787	2	O56293_9BETA	O56293	human herpe
364	31	75.6	790	2	Q91BF7_NPVST	Q91bf7	spodoptera
365	31	75.6	815	2	Q6D1H2_ERWCT	Q6dlh2	erwinia car
366	31	75.6	816	2	Q80VG8_MOUSE	Q80vg8	mus musculu
367	31	75.6	836	2	Q9VUH8_DROME	Q9vuh8	drosophila
368	31	75.6	840	2	Q4Q6N4_LEIMA	Q4q6n4	leishmania
369	31	75.6	849	2	Q571E8_MOUSE	Q571e8	mus musculu
370	31	75.6	881	1	GAL4_YEAST	P04386	saccharomyc
371	31	75.6	881	2	Q76MW9_DROME	Q76mw9	drosophila
372	31	75.6	881	2	Q4QJH2_LEIMA	Q4qjh2	leishmania
373	31	75.6	908	2	Q7TME6_MOUSE	Q7tme6	mus musculu
374	31	75.6	910	2	Q7TME8_MOUSE	Q7tme8	mus musculu
375	31	75.6	910	2	Q7TME9_MOUSE	Q7tme9	mus musculu
376	31	75.6	910	2	Q5QNT4_MOUSE	Q5qnt4	mus musculu
377	31	75.6	910	2	Q8CB82_MOUSE	Q8cb82	mus musculu
378	31	75.6	911	2	Q8B661_ADET1	Q8b661	tree shrew
379	31	75.6	932	2	Q695S2_9ADEN	Q695s2	simian aden
380	31	75.6	932	2	Q6QPA4_9ADEN	Q6qpa4	simian aden
381	31	75.6	933	2	Q6QPH6_9ADEN	Q6qph6	simian aden
382	31	75.6	933	2	Q8UY79_9ADEN	Q8uy79	simian aden
383	31	75.6	935	2	Q80RH9_ADE04	Q80rh9	human adeno
384	31	75.6	936	2	Q5GFA8_ADE04	Q5gfa8	human adeno
385	31	75.6	936	2	Q67814_ADE04	Q67814	human adeno
386	31	75.6	936	2	Q9YVE4_ADE04	Q9yve4	human adeno
387	31	75.6	936	2	Q9YVE5_ADE04	Q9yve5	human adeno
388	31	75.6	936	2	Q9YVE6_ADE04	Q9yve6	human adeno
389	31	75.6	936	2	Q6H1C4_9ADEN	Q6h1c4	human adeno
390	31	75.6	936	2	Q5VHB3_ADE04	Q5vhb3	human adeno
391	31	75.6	942	2	Q6QPE0_9ADEN	Q6qpe0	simian aden
392	31	75.6	946	2	Q54V63_DICDI	Q54v63	dictyosteli
393	31	75.6	947	2	Q83109_9ADEN	Q83109	human adeno
394	31	75.6	947	2	Q4KSJ8_9ADEN	Q4ksj8	human adeno
395	31	75.6	949	2	Q914F4_9ADEN	Q914f4	human adeno
396	31	75.6	949	2	Q9DT29_9ADEN	Q9dt29	human adeno
397	31	75.6	949	2	Q9WKD3_9ADEN	Q9wkd3	unidentifie
398	31	75.6	951	1	HEX_ADE05	P04133	human adeno
399	31	75.6	952	2	Q6VGU6_9ADEN	Q6vgu6	human adeno
400	31	75.6	952	2	Q805J1_ADE05	Q805j1	human adeno
401	31	75.6	952	2	Q80RI0_ADE05	Q80ri0	human adeno
402	31	75.6	952	2	Q80RI5_ADE05	Q80ri5	human adeno
403	31	75.6	952	2	Q80RJ2_ADE05	Q80rj2	human adeno
404	31	75.6	953	1	HEX_ADE09	P36853	human adeno
405	31	75.6	963	2	Q6R5M3_ADE01	Q6r5m3	feline aden
406	31	75.6	964	2	Q71BW8_ADE01	Q71bw8	human adeno
407	31	75.6	967	1	HEX_ADE02	P03277	human adeno
408	31	75.6	968	2	Q7TEH9_ADE02	Q7teh9	human adeno
409	31	75.6	968	2	Q7TEI0_ADE02	Q7tei0	human adeno
410	31	75.6	968	2	Q80RI1_ADE02	Q80ri1	human adeno
411	31	75.6	968	2	Q80RI3_ADE02	Q80ri3	human adeno
412	31	75.6	968	2	Q910Z8_ADE02	Q910z8	human adeno
413	31	75.6	968	2	Q912J7_ADE02	Q912j7	human adeno
414	31	75.6	968	2	Q564J3_ADE02	Q564j3	human adeno

415	31	75.6	969	2	Q910Z9_ADE02	Q910z9 human adeno
416	31	75.6	1014	2	Q6ZU69_HUMAN	Q6zu69 homo sapien
417	31	75.6	1081	2	Q5TN36_ANOGA	Q5tn36 anopheles g
418	31	75.6	1113	2	Q4RJK1_TETNG	Q4rjk1 tetraodon n
419	31	75.6	1150	2	Q50ND1_ENTHI	Q50nd1 entamoeba h
420	31	75.6	1154	2	Q4J2R1_AZOVI	Q4j2r1 azotobacter
421	31	75.6	1158	2	Q9CSS1_MOUSE	Q9css1 mus musculu
422	31	75.6	1176	2	Q7SG26_NEUCR	Q7sg26 neurospora
423	31	75.6	1208	2	Q6FSL9_CANGA	Q6fsl9 candida gla
424	31	75.6	1262	2	Q4QC72_LEIMA	Q4qc72 leishmania
425	31	75.6	1305	2	Q6FPD2_CANGA	Q6fpd2 candida gla
426	31	75.6	1371	2	Q6PDI7_MOUSE	Q6pdi7 mus musculu
427	31	75.6	1422	2	Q8DIE5_SYNEL	Q8die5 synechococc
428	31	75.6	1461	2	Q6ZPE9_MOUSE	Q6zpe9 mus musculu
429	31	75.6	1469	2	Q4QDQ7_LEIMA	Q4qdq7 leishmania
430	31	75.6	1832	2	Q4WD95_ASPFU	Q4wd95 aspergillus
431	31	75.6	1966	2	Q9NHX6_DROME	Q9nhx6 drosophila
432	31	75.6	1966	2	Q8IQA6_DROME	Q8iqa6 drosophila
433	31	75.6	1985	2	Q9VSK5_DROME	Q9vsk5 drosophila
434	31	75.6	1985	2	Q8T9N4_DROME	Q8t9n4 drosophila
435	31	75.6	1985	2	Q7KUA8_DROME	Q7kua8 drosophila
436	31	75.6	1987	2	Q5WRT9_CAEEL	Q5wrt9 caenorhabdi
437	31	75.6	1988	2	Q86BH2_DROME	Q86bh2 drosophila
438	31	75.6	2030	2	Q747P6_GEOSL	Q747p6 geobacter s
439	31	75.6	2157	2	Q8TGD8_ASPTE	Q8tgd8 aspergillus
440	31	75.6	2512	2	Q10896_MYCTU	Q10896 mycobacteri
441	31	75.6	2512	2	Q7U2U9_MYCBO	Q7u2u9 mycobacteri
442	31	75.6	2520	2	Q7DAG9_MYCTU	Q7dag9 mycobacteri
443	31	75.6	2954	2	Q4IRV3_GIBZE	Q4irv3 gibberella
444	31	75.6	4065	1	TOM1_NEUCR	Q9p4z1 neurospora
445	30	73.2	64	2	Q7Y3Q9_9CAUD	Q7y3q9 enterobacte
446	30	73.2	85	2	Q7QRL2_GIALA	Q7qrl2 giardia lam
447	30	73.2	91	2	Q9R655_AZOVI	Q9r655 azotobacter
448	30	73.2	98	2	Q98TL5_PLAFE	Q98tl5 platichthys
449	30	73.2	101	2	Q8ZHM5_YERPE	Q8zhm5 yersinia pe
450	30	73.2	101	2	Q666Y4_YERPS	Q666y4 yersinia ps
451	30	73.2	102	2	Q6WGG6_ADEB2	Q6wgg6 bovine aden
452	30	73.2	109	2	Q880I2_PSESM	Q880i2 pseudomonas
453	30	73.2	113	2	Q4ZRZ8_PSESY	Q4zrz8 pseudomonas
454	30	73.2	119	1	VTU3_DROME	Q06521 drosophila
455	30	73.2	133	1	EXDL2_HELPJ	P64102 helicobacte
456	30	73.2	133	1	EXDL2_HELPY	P64101 helicobacte
457	30	73.2	136	2	Q4XHX4_PLACH	Q4xhx4 plasmodium
458	30	73.2	137	2	Q7RPV3_PLAYO	Q7rpv3 plasmodium
459	30	73.2	144	1	APD22_APIME	P35581 apis mellif
460	30	73.2	145	2	Q932T3_STREQ	Q932t3 streptococc
461	30	73.2	145	2	Q932U2_STREQ	Q932u2 streptococc
462	30	73.2	145	2	Q93PG0_STREQ	Q93pg0 streptococc
463	30	73.2	145	2	Q93PG1_STREQ	Q93pg1 streptococc
464	30	73.2	145	2	Q93PG2_STREQ	Q93pg2 streptococc
465	30	73.2	145	2	Q93PG3_STREQ	Q93pg3 streptococc
466	30	73.2	145	2	Q93PG4_STREQ	Q93pg4 streptococc
467	30	73.2	145	2	Q93PG5_STREQ	Q93pg5 streptococc
468	30	73.2	149	2	Q5TUC5_ANOGA	Q5tuc5 anopheles g
469	30	73.2	154	2	Q9XVC1_CAEEL	Q9xvc1 caenorhabdi
470	30	73.2	155	2	Q4WXS1_ASPFU	Q4wxs1 aspergillus
471	30	73.2	155	2	Q8PGQ2_XANAC	Q8pgq2 xanthomonas

472	30	73.2	155	2	Q7TG29_9CALI	Q7tg29	human calic
473	30	73.2	156	2	Q4XYQ9_PLACH	Q4xyq9	plasmodium
474	30	73.2	157	2	Q962L7_PLAVI	Q962l7	plasmodium
475	30	73.2	160	1	Y535_CHLTR	O84540	chlamydia t
476	30	73.2	160	2	Q8DGE0_SYNEL	Q8dge0	synechococc
477	30	73.2	160	2	Q8CBL2_MOUSE	Q8cbl2	mus musculu
478	30	73.2	163	2	O77315_PLAF7	O77315	plasmodium
479	30	73.2	168	1	APD14_APIME	Q06601	apis mellif
480	30	73.2	175	2	Q4F9N3_9NEOP	Q4f9n3	gorgopis li
481	30	73.2	177	2	Q605C7_METCA	Q605c7	methylococc
482	30	73.2	177	2	Q8EK54_SHEON	Q8ek54	shewanella
483	30	73.2	177	2	Q9CL45_PASMU	Q9cl45	pasteurella
484	30	73.2	181	2	Q73TT0_MYCPA	Q73tt0	mycobacteri
485	30	73.2	183	2	P74481_SYNY3	P74481	synechocyst
486	30	73.2	184	2	Q9A6L5_CAUCR	Q9a6l5	caulobacter
487	30	73.2	185	2	Q4GWU1_MYCSM	Q4gwu1	mycobacteri
488	30	73.2	187	2	Q6MFC8_NEUCR	Q6mfc8	neurospora
489	30	73.2	188	2	Q614N0_CAEBR	Q614n0	caenorhabdi
490	30	73.2	192	2	Q59NY0_CANAL	Q59ny0	candida alb
491	30	73.2	192	2	Q9UFJ8_HUMAN	Q9ufj8	homo sapien
492	30	73.2	196	2	Q4IJ64_GIBZE	Q4ij64	gibberella
493	30	73.2	199	2	Q8WSY8_APIME	Q8wsy8	apis mellif
494	30	73.2	200	2	Q92ZM8_RHIME	Q92zm8	rhizobium m
495	30	73.2	200	2	Q8U862_AGRT5	Q8u862	agrobacteri
496	30	73.2	217	2	Q8YJZ0_ANASP	Q8yjjz0	anabaena sp
497	30	73.2	219	2	Q9K6I8_BACHD	Q9k6i8	bacillus ha
498	30	73.2	224	2	Q4KBQ8_PSEF5	Q4kbq8	pseudomonas
499	30	73.2	226	2	Q8RWK9_ARATH	Q8rwk9	arabidopsis
500	30	73.2	238	2	Q9FPE1_ARATH	Q9fpe1	arabidopsis
501	30	73.2	240	2	Q821U1_CHLCV	Q821u1	chlamydophi
502	30	73.2	240	2	Q9DFM3_GILMI	Q9dfm3	gillichthys
503	30	73.2	243	2	Q6ADA4_LEIXX	Q6ada4	leifsonia x
504	30	73.2	244	2	Q8L3T0_ARATH	Q8l3t0	arabidopsis
505	30	73.2	250	2	Q4U8J3_THEAN	Q4u8j3	theileria a
506	30	73.2	251	2	Q6RYF1_HORVD	Q6ryf1	hordeum vul
507	30	73.2	254	2	Q6PX45_TRIMO	Q6px45	triticum mo
508	30	73.2	254	2	Q8UH29_AGRT5	Q8uh29	agrobacteri
509	30	73.2	257	2	Q4NT42_9DELT	Q4nt42	anaeromyxob
510	30	73.2	258	2	O32585_ECOLI	O32585	escherichia
511	30	73.2	258	2	Q5IQZ3_9ESCH	Q5iqz3	escherichia
512	30	73.2	258	2	Q5IQZ5_SHIBO	Q5iqz5	shigella bo
513	30	73.2	258	2	Q5IQZ8_SHIBO	Q5iqz8	shigella bo
514	30	73.2	258	2	Q6UPC3_ECOLI	Q6upc3	escherichia
515	30	73.2	258	2	Q8GJ13_ECOLI	Q8gj13	escherichia
516	30	73.2	259	2	Q54MW4_DICDI	Q54mw4	dictyosteli
517	30	73.2	259	2	Q8XZH6_RALSO	Q8xzh6	ralstonia s
518	30	73.2	260	2	Q64W86_BACFR	Q64w86	bacteroides
519	30	73.2	261	2	Q6AC64_LEIXX	Q6ac64	leifsonia x
520	30	73.2	262	2	Q4WIM4_ASPFU	Q4wim4	aspergillus
521	30	73.2	265	2	Q7YQN1_DIDMA	Q7yqn1	didelphis m
522	30	73.2	272	2	Q9ZI16_STRLI	Q9zi16	streptomyce
523	30	73.2	272	2	Q9L025_STRCO	Q9l025	streptomyce
524	30	73.2	272	2	Q8UIA3_AGRT5	Q8uia3	agrobacteri
525	30	73.2	274	2	Q4Sjq5_TETNG	Q4sjq5	tetraodon n
526	30	73.2	275	2	Q7S5B1_NEUCR	Q7s5b1	neurospora
527	30	73.2	278	2	Q9FD25_NOSS9	Q9fd25	nostoc sp.
528	30	73.2	283	1	APD73_APIME	Q06602	apis mellif

529	30	73.2	283	2	Q60M11_CAEBR	Q60m11	caenorhabdi
530	30	73.2	284	2	Q18784_CAEEL	Q18784	caenorhabdi
531	30	73.2	284	2	Q92RN5_RHIME	Q92rn5	rhizobium m
532	30	73.2	285	2	O82166_ARATH	O82166	arabidopsis
533	30	73.2	288	2	Q9SIY4_ARATH	Q9siy4	arabidopsis
534	30	73.2	288	2	Q66IS5_XENLA	Q66is5	xenopus lae
535	30	73.2	289	2	Q7WCD7_BORPA	Q7wcd7	bordetella
536	30	73.2	289	2	Q7WQE3_BORBR	Q7wqe3	bordetella
537	30	73.2	292	2	Q7TSX4_RAT	Q7tsx4	rattus norv
538	30	73.2	298	2	Q7D0I5_AGR5	Q7d0i5	agrobacteri
539	30	73.2	300	1	SPSY_YEAST	Q12455	saccharomyc
540	30	73.2	300	2	Q5K8B9_CRYNE	Q5k8b9	cryptococcu
541	30	73.2	302	2	Q9YJJ8_9REOV	Q9yjj8	banna virus
542	30	73.2	302	2	Q9YWN4_9REOV	Q9ywn4	banna virus
543	30	73.2	302	2	Q9YWP0_9REOV	Q9ywp0	banna virus
544	30	73.2	303	2	Q55MF5_CRYNE	Q55mf5	cryptococcu
545	30	73.2	305	2	Q4XW02_PLACH	Q4xw02	plasmodium
546	30	73.2	306	2	Q9FG52_ARATH	Q9fg52	arabidopsis
547	30	73.2	308	2	Q8UC89_AGR5	Q8uc89	agrobacteri
548	30	73.2	322	1	Y367_MYCPN	P75414	mycoplasma
549	30	73.2	324	2	Q9KH35_PANAY	Q9kh35	pantoea agg
550	30	73.2	330	2	Q5A1D6_CANAL	Q5ald6	candida alb
551	30	73.2	330	2	Q8G6H0_BIFLO	Q8g6h0	bifidobacte
552	30	73.2	330	2	Q8UDX8_AGR5	Q8udx8	agrobacteri
553	30	73.2	331	2	Q57DA8_BRUAB	Q57da8	brucella ab
554	30	73.2	331	2	Q8YH41_BRUME	Q8yh41	brucella me
555	30	73.2	339	2	Q40062_HORVU	Q40062	hordeum vul
556	30	73.2	339	2	Q7ZUX2_BRARE	Q7zux2	brachydanio
557	30	73.2	340	2	Q4WWE5_ASPFU	Q4wwe5	aspergillus
558	30	73.2	342	2	Q7CY47_AGR5	Q7cy47	agrobacteri
559	30	73.2	343	2	Q9HF07_CANAL	Q9hf07	candida alb
560	30	73.2	346	2	Q4FVT9_LEIMA	Q4fvt9	leishmania
561	30	73.2	347	2	Q4IPX9_GIBZE	Q4ipx9	gibberella
562	30	73.2	349	2	Q857A3_9CAUD	Q857a3	mycobacteri
563	30	73.2	353	2	O42253_CHICK	O42253	gallus gall
564	30	73.2	358	2	Q9VHZ8_DROME	Q9vzh8	drosophila
565	30	73.2	359	2	Q4KJ79_PSEF5	Q4kj79	pseudomonas
566	30	73.2	362	2	Q9LHT4_ARATH	Q9lht4	arabidopsis
567	30	73.2	367	1	DUS1_HUMAN	P28562	homo sapien
568	30	73.2	367	1	DUS1_MOUSE	P28563	mus musculu
569	30	73.2	367	1	DUS1_RAT	Q64623	rattus norv
570	30	73.2	367	2	Q63683_RAT	Q63683	rattus norv
571	30	73.2	367	2	Q548G6_RAT	Q548g6	rattus norv
572	30	73.2	369	2	Q90W58_XENLA	Q90w58	xenopus lae
573	30	73.2	369	2	Q91790_XENLA	Q91790	xenopus lae
574	30	73.2	369	2	Q6GLD5_XENTR	Q6gld5	xenopus tro
575	30	73.2	369	2	Q5U4X4_XENLA	Q5u4x4	xenopus lae
576	30	73.2	378	2	Q84ME1_ARATH	Q84me1	arabidopsis
577	30	73.2	378	2	Q8L7V9_ARATH	Q8l7v9	arabidopsis
578	30	73.2	382	2	Q86MV8_9TRYP	Q86mv8	trypanosoma
579	30	73.2	383	2	Q4P7H6_USTMA	Q4p7h6	ustilago ma
580	30	73.2	386	2	Q7NMP1_GLOVI	Q7nmp1	gloeobacter
581	30	73.2	392	2	Q9KH97_AZOVI	Q9kh97	azotobacter
582	30	73.2	392	2	Q93M80_9GAMM	Q93m80	azotobacter
583	30	73.2	392	2	Q4J5T4_AZOVI	Q4j5t4	azotobacter
584	30	73.2	392	2	Q6FYQ0_BARQU	Q6fyq0	bartonella
585	30	73.2	395	2	Q5XAN8_STRP6	Q5xan8	streptococc

586	30	73.2	395	2	Q99YM2_STRPY	Q99ym2 streptococc
587	30	73.2	395	2	Q8NZZ8_STRP8	Q8nzz8 streptococc
588	30	73.2	395	2	Q8K6E5_STRP3	Q8k6e5 streptococc
589	30	73.2	396	2	Q96IK6_HUMAN	Q96ik6 homo sapien
590	30	73.2	397	1	ATG5_NEUCR	Q872c6 neurospora
591	30	73.2	398	2	Q56CY6_9CUCU	Q56cy6 dendroctonu
592	30	73.2	399	2	Q6IR65_XENLA	Q6ir65 xenopus lae
593	30	73.2	399	2	Q5M7N3_XENTR	Q5m7n3 xenopus tro
594	30	73.2	402	2	Q759U9_ASHGO	Q759u9 ashbya goss
595	30	73.2	403	2	Q7QWK4_GIALA	Q7qwk4 giardia lam
596	30	73.2	405	2	Q4LG48_BOMMO	Q4lg48 bombyx mori
597	30	73.2	407	2	Q8NBT0_HUMAN	Q8nbt0 homo sapien
598	30	73.2	407	2	Q89DL5_BRAJA	Q89dl5 bradyrhizob
599	30	73.2	411	2	Q9ZKM1_HELPJ	Q9zkm1 helicobacte
600	30	73.2	419	2	Q8PYC9_METMA	Q8pyc9 methanosarc
601	30	73.2	419	2	Q8TJ11_METAC	Q8tj11 methanosarc
602	30	73.2	422	2	Q4RKE1_TETNG	Q4rke1 tetraodon n
603	30	73.2	423	2	Q5FUT7_GLUOX	Q5fut7 gluconobact
604	30	73.2	426	2	Q64FZ5_MUSPF	Q64fz5 mustela put
605	30	73.2	426	2	Q6DT31_MUSER	Q6dt31 mustela erm
606	30	73.2	426	2	Q8H407_ORYSA	Q8h407 oryza sativ
607	30	73.2	427	2	Q4IWZ0_AZOVI	Q4iwz0 azotobacter
608	30	73.2	435	1	ZFNL5_ARATH	Q5rjc5 arabidopsis
609	30	73.2	437	2	Q4WB17_ASPFU	Q4wb17 aspergillus
610	30	73.2	439	2	Q60SH9_CAEBR	Q60sh9 caenorhabdi
611	30	73.2	443	2	Q5LWB4_SILPO	Q5lwb4 silicibacte
612	30	73.2	449	2	Q4MVB3_BACCE	Q4mvp3 bacillus ce
613	30	73.2	449	2	Q6HC86_BACHK	Q6hc86 bacillus th
614	30	73.2	449	2	Q72YS2_BACC1	Q72ys2 bacillus ce
615	30	73.2	449	2	Q816N3_BACCR	Q816n3 bacillus ce
616	30	73.2	449	2	Q81KF0_BACAN	Q81kf0 bacillus an
617	30	73.2	449	2	Q632P5_BACCZ	Q632p5 bacillus ce
618	30	73.2	457	2	Q4LRT0_9BURK	Q4lrt0 burkholderi
619	30	73.2	457	2	Q62GP2_BURMA	Q62gp2 burkholderi
620	30	73.2	459	2	Q4ZZH9_PSESY	Q4zzh9 pseudomonas
621	30	73.2	462	2	Q984H6_RHILO	Q984h6 rhizobium l
622	30	73.2	467	2	Q63PX7_BURPS	Q63px7 burkholderi
623	30	73.2	470	1	PROP_CAVPO	Q64181 cavia porce
624	30	73.2	474	2	Q8FQA4_COREF	Q8fqa4 corynebacte
625	30	73.2	486	2	Q7VSP3_BORPE	Q7vsp3 bordetella
626	30	73.2	486	2	Q7W373_BORPA	Q7w373 bordetella
627	30	73.2	486	2	Q7WEJ2_BORBR	Q7wej2 bordetella
628	30	73.2	488	1	PE2R4_HUMAN	P35408 homo sapien
629	30	73.2	488	1	PE2R4_RAT	P43114 rattus norrv
630	30	73.2	488	2	Q91VE4_MOUSE	Q91ve4 mus musculu
631	30	73.2	488	2	Q6P0U7_BRARE	Q6p0u7 brachydanio
632	30	73.2	490	1	PE2R4_PANTR	Q95kz0 pan troglod
633	30	73.2	490	2	Q7JGJ7_PAPHU	Q7jgj7 papio hamad
634	30	73.2	490	2	Q95J39_MACFA	Q95j39 macaca fasc
635	30	73.2	490	2	Q4R6E1_MACFA	Q4r6e1 macaca fasc
636	30	73.2	490	2	Q9W6G5_BRARE	Q9w6g5 brachydanio
637	30	73.2	491	2	Q5VKR2_SACER	Q5vkr2 saccharopol
638	30	73.2	492	2	Q8MJ08_BOVIN	Q8mj08 bos taurus
639	30	73.2	492	2	Q9TU16_CANFA	Q9tu16 canis famil
640	30	73.2	497	1	IRF5_MOUSE	P56477 mus musculu
641	30	73.2	501	2	Q5ZE12_ORYSA	Q5ze12 oryza sativ
642	30	73.2	502	2	Q8WPX2_PARLI	Q8wpx2 paracentrot

643	30	73.2	504	2	Q6BDA4_9POAL	Q6bda4	zoysia tenu
644	30	73.2	508	2	Q8FP11_COREF	Q8fp11	corynebacte
645	30	73.2	509	2	Q4NC61_9MICC	Q4nc61	arthrobacte
646	30	73.2	513	1	PE2R4_MOUSE	P32240	mus musculu
647	30	73.2	516	2	O80726_ARATH	O80726	arabidopsis
648	30	73.2	516	2	Q8RY31_ARATH	Q8ry31	arabidopsis
649	30	73.2	521	2	Q55BM9_DICDI	Q55bm9	dictyosteli
650	30	73.2	524	2	Q4L9K9_STAHJ	Q4l9k9	staphylococ
651	30	73.2	533	2	Q4WDU7_ASPFU	Q4wdu7	aspergillus
652	30	73.2	552	1	FLIF_ECOLI	P25798	escherichia
653	30	73.2	552	2	Q8X045_NEUCR	Q8x045	neurospora
654	30	73.2	552	2	Q8FGL0_ECOL6	Q8fgl0	escherichia
655	30	73.2	552	2	Q8XBB0_ECO57	Q8xbb0	escherichia
656	30	73.2	562	2	Q8QL25_9VIRU	Q8ql25	sulfolobus
657	30	73.2	564	2	Q7PWK8_ANOGA	Q7pwk8	anopheles g
658	30	73.2	565	1	DSBD_ECO57	P58162	escherichia
659	30	73.2	565	1	DSBD_ECOLI	P36655	escherichia
660	30	73.2	565	2	Q8CVH5_ECOL6	Q8cvh5	escherichia
661	30	73.2	567	2	Q8V9N0_9VIRU	Q8v9n0	sulfolobus
662	30	73.2	570	2	Q7RXV4_NEUCR	Q7rxv4	neurospora
663	30	73.2	570	2	Q8ZF86_YERPE	Q8zf86	yersinia pe
664	30	73.2	570	2	Q66BR7_YERPS	Q66br7	yersinia ps
665	30	73.2	572	2	Q8UGH0_AGRT5	Q8ugh0	agrobacteri
666	30	73.2	579	2	Q6CBP0_YARLI	Q6cbp0	yarrowia li
667	30	73.2	580	2	Q5TJ88_9VIRU	Q5tj88	sulfolobus
668	30	73.2	582	2	Q5FBG7_GIBZE	Q5fbg7	gibberella
669	30	73.2	582	2	Q4IRR1_GIBZE	Q4irr1	gibberella
670	30	73.2	583	2	Q5JFZ9_PYRKO	Q5j fz9	pyrococcus
671	30	73.2	587	2	Q5V032_HALMA	Q5v032	haloarcula
672	30	73.2	593	2	Q7D017_AGRT5	Q7d017	agrobacteri
673	30	73.2	604	2	Q8G6V3_BIFLO	Q8g6v3	bifidobacte
674	30	73.2	608	1	SEC9_YARLI	Q6c5g0	yarrowia li
675	30	73.2	628	1	BGAL_LACHE	Q7wtb4	lactobacill
676	30	73.2	628	2	Q5UU95_LACHE	Q5uu95	lactobacill
677	30	73.2	629	2	Q6MW02_NEUCR	Q6mw02	neurospora
678	30	73.2	632	1	YOT7_CAEEL	P34653	caenorhabdi
679	30	73.2	633	2	Q96LN8_HUMAN	Q96ln8	homo sapien
680	30	73.2	634	2	Q17474_CAEEL	Q17474	caenorhabdi
681	30	73.2	634	2	Q17475_CAEEL	Q17475	caenorhabdi
682	30	73.2	634	2	Q8YPA0_ANASP	Q8ypa0	anabaena sp
683	30	73.2	638	2	O32924_MYCLE	O32924	mycobacteri
684	30	73.2	639	2	Q96X24_YARLI	Q96x24	yarrowia li
685	30	73.2	642	2	Q6BQJ8_DEBHA	Q6bqj8	debaryomyce
686	30	73.2	645	2	Q6CTH5_KLULA	Q6cth5	kluveromyce
687	30	73.2	655	2	Q4H3K9_CIOIN	Q4h3k9	ciona intes
688	30	73.2	660	2	Q61J16_CAEBR	Q61j16	caenorhabdi
689	30	73.2	667	2	Q74HC7_LACJO	Q74hc7	lactobacill
690	30	73.2	673	2	Q8VBK5_ADE07	Q8vbk5	human adeno
691	30	73.2	674	1	DCMB_MOOTH	P27989	moorella th
692	30	73.2	677	2	Q838N2_ENTFA	Q838n2	enterococcu
693	30	73.2	678	2	Q803F8_BRARE	Q803f8	brachydanio
694	30	73.2	679	2	Q4HUU2_GIBZE	Q4huu2	gibberella
695	30	73.2	679	2	Q62BV1_BURMA	Q62bv1	burkholderi
696	30	73.2	681	1	DPO3X_MYCPN	P75177	mycoplasma
697	30	73.2	688	2	Q9GNP2_CIOSA	Q9gnp2	ciona savig
698	30	73.2	695	2	Q8KCV9_CHLTE	Q8kcv9	chlorobium
699	30	73.2	697	2	Q6G142_BARQU	Q6g142	bartonella

700	30	73.2	712	2	Q4IGJ0_GIBZE	Q4igj0	gibberella
701	30	73.2	721	2	Q59L34_CANAL	Q59l34	candida alb
702	30	73.2	722	1	COAT_PAVHH	P03136	hamster par
703	30	73.2	730	2	P96090_THEBR	P96090	thermoanaer
704	30	73.2	746	2	Q4IAI1_GIBZE	Q4iaai1	gibberella
705	30	73.2	746	2	Q52AQ6_MAGGR	Q52aq6	magnaporth
706	30	73.2	753	2	Q6PFP4_BRARE	Q6pfp4	brachydanio
707	30	73.2	757	2	Q98FC7_RHILO	Q98fc7	rhizobium l
708	30	73.2	766	2	Q662B3_BORGA	Q662b3	borrelia ga
709	30	73.2	770	2	Q9GNP1_CIOSA	Q9gnp1	ciona savig
710	30	73.2	780	1	T22D2_HUMAN	O75157	homo sapien
711	30	73.2	784	2	Q9JRQ1_THEET	Q9jrq1	thermoanaer
712	30	73.2	800	2	Q6CMP0_KLULA	Q6cmp0	kluveromyc
713	30	73.2	814	1	ECM22_YEAST	Q05958	saccharomyc
714	30	73.2	815	2	Q758K7_ASHGO	Q758k7	ashbya goss
715	30	73.2	821	1	AP1G1_HUMAN	O43747	homo sapien
716	30	73.2	821	1	EPS8_MOUSE	Q08509	mus musculu
717	30	73.2	821	2	Q63LI6_BURPS	Q63li6	burkholderi
718	30	73.2	822	2	Q5R5M2_PONPY	Q5r5m2	pongo pygma
719	30	73.2	823	2	Q8G7R6_BIFLO	Q8g7r6	bifidobacte
720	30	73.2	825	2	Q8IY97_HUMAN	Q8iy97	homo sapien
721	30	73.2	829	1	CADH3_HUMAN	P22223	homo sapien
722	30	73.2	829	2	Q9HE91_NEUCR	Q9he91	neurospora
723	30	73.2	847	2	Q870M7_YARLI	Q870m7	yarrowia li
724	30	73.2	847	2	Q6C4C4_YARLI	Q6c4c4	yarrowia li
725	30	73.2	855	1	GAF1_SCHPO	Q10280	schizosacch
726	30	73.2	861	2	Q8UGU8_AGR5	Q8ugu8	agrobacteri
727	30	73.2	868	1	SPO75_YEAST	Q07798	saccharomyc
728	30	73.2	869	2	Q9I4H4_PSEAE	Q9i4h4	pseudomonas
729	30	73.2	875	2	Q4S2I4_TETNG	Q4s2i4	tetraodon n
730	30	73.2	889	2	Q8YS17_ANASP	Q8ys17	anabaena sp
731	30	73.2	889	2	Q5FWU7_XENLA	Q5fwu7	xenopus lae
732	30	73.2	895	2	Q521W6_MAGGR	Q521w6	magnaporth
733	30	73.2	898	2	Q61FV6_CAEBR	Q61fv6	caenorhabdi
734	30	73.2	905	1	HEX_ADECC	Q65955	canine aden
735	30	73.2	905	1	HEX_ADECR	O39619	canine aden
736	30	73.2	905	2	P87562_ADEC2	P87562	canine aden
737	30	73.2	908	2	Q8W4G4_ARATH	Q8w4g4	arabidopsis
738	30	73.2	908	2	Q9LVX1_ARATH	Q9lvx1	arabidopsis
739	30	73.2	910	2	Q994D9_9ADEN	Q994d9	porcine ade
740	30	73.2	914	2	Q61GL2_CAEBR	Q61gl2	caenorhabdi
741	30	73.2	919	2	Q5KJ83_CRYNE	Q5kj83	cryptococcu
742	30	73.2	920	2	Q516C7_ENTHI	Q516c7	entamoeba h
743	30	73.2	924	2	Q55T59_CRYNE	Q55t59	cryptococcu
744	30	73.2	926	2	Q8YZM5_ANASP	Q8yzm5	anabaena sp
745	30	73.2	933	2	Q4U1I6_BRARE	Q4uli6	brachydanio
746	30	73.2	934	2	O91858_ADE07	O91858	human adeno
747	30	73.2	934	2	Q8JQA5_ADE07	Q8jqa5	human adeno
748	30	73.2	934	2	Q9YVD9_ADE07	Q9yvd9	human adeno
749	30	73.2	934	2	Q9YVE0_ADE07	Q9yve0	human adeno
750	30	73.2	934	2	Q9YVE1_ADE07	Q9yve1	human adeno
751	30	73.2	934	2	Q9YIE0_ADE07	Q9yie0	human adeno
752	30	73.2	934	2	Q6RK87_ADE07	Q6rk87	human adeno
753	30	73.2	937	1	HEX_ADE07	P36851	human adeno
754	30	73.2	937	2	Q9YVE2_ADE07	Q9yve2	human adeno
755	30	73.2	938	2	Q9W8S1_ADEP3	Q9w8s1	porcine ade
756	30	73.2	939	1	HEX_ADEP3	Q9ytr8	porcine ade

757	30	73.2	939	2	Q84178_ADEP3	Q84178 porcine ade
758	30	73.2	940	1	HEX_ADE16	P36854 human adeno
759	30	73.2	942	2	Q6Y8G7_BRARE	Q6y8g7 brachydanio
760	30	73.2	942	2	Q502S8_BRARE	Q502s8 brachydanio
761	30	73.2	944	1	HEX_ADE03	P36849 human adeno
762	30	73.2	944	2	Q5FX77_ADE03	Q5fx77 human adeno
763	30	73.2	944	2	Q805P5_ADE03	Q805p5 human adeno
764	30	73.2	944	2	Q80RH6_ADE03	Q80rh6 human adeno
765	30	73.2	944	2	Q80RH7_ADE03	Q80rh7 human adeno
766	30	73.2	944	2	Q80RH8_ADE03	Q80rh8 human adeno
767	30	73.2	944	2	Q80RI2_ADE05	Q80ri2 human adeno
768	30	73.2	944	2	Q80RI4_ADE03	Q80ri4 human adeno
769	30	73.2	944	2	Q80RI6_ADE03	Q80ri6 human adeno
770	30	73.2	944	2	Q80RI7_ADE03	Q80ri7 human adeno
771	30	73.2	944	2	Q80RI8_ADE03	Q80ri8 human adeno
772	30	73.2	944	2	Q80RI9_ADE03	Q80ri9 human adeno
773	30	73.2	944	2	Q80RJ0_ADE03	Q80rj0 human adeno
774	30	73.2	944	2	Q80RJ1_ADE03	Q80rj1 human adeno
775	30	73.2	944	2	Q80RJ3_ADE03	Q80rj3 human adeno
776	30	73.2	944	2	Q80RJ4_ADE03	Q80rj4 human adeno
777	30	73.2	944	2	Q80RJ5_ADE03	Q80rj5 human adeno
778	30	73.2	944	2	Q80RJ6_ADE03	Q80rj6 human adeno
779	30	73.2	944	2	Q80RJ7_ADE03	Q80rj7 human adeno
780	30	73.2	944	2	Q4F931_9ADEN	Q4f931 human adeno
781	30	73.2	944	2	Q4F7E7_9ADEN	Q4f7e7 human adeno
782	30	73.2	948	2	Q91Y17_MOUSE	Q91y17 mus musculu
783	30	73.2	948	2	Q5UW08_9ADEN	Q5uw08 human adeno
784	30	73.2	948	2	Q8B8T3_9ADEN	Q8b8t3 human adeno
785	30	73.2	951	2	Q5CXN5_CRYPV	Q5cxn5 cryptospori
786	30	73.2	951	2	Q9DT30_9ADEN	Q9dt30 human adeno
787	30	73.2	952	2	Q7T936_ADE35	Q7t936 human adeno
788	30	73.2	952	2	Q99I74_ADE35	Q99i74 human adeno
789	30	73.2	959	2	Q7SB57_NEUCR	Q7sb57 neurospora
790	30	73.2	963	2	Q75FA6_ASHGO	Q75fa6 ashbya goss
791	30	73.2	974	2	Q20143_CAEEL	Q20143 caenorhabdi
792	30	73.2	990	2	Q560K8_CRYNE	Q560k8 cryptococcu
793	30	73.2	999	2	Q5CII2_CRYHO	Q5cii2 cryptospori
794	30	73.2	1000	2	Q51YH4_MAGGR	Q51yh4 magnaporthe
795	30	73.2	1003	2	Q8EUZ4_MYCPE	Q8euz4 mycoplasma
796	30	73.2	1007	2	Q9ZVD4_ARATH	Q9zvd4 arabidopsis
797	30	73.2	1014	2	Q8Y0K3_RALSO	Q8y0k3 ralstonia s
798	30	73.2	1020	2	Q9C0D4_HUMAN	Q9c0d4 homo sapien
799	30	73.2	1053	2	Q7S0N8_NEUCR	Q7s0n8 neurospora
800	30	73.2	1149	2	Q64J84_9CORY	Q64j84 corynebacte
801	30	73.2	1155	2	Q5CNI4_CRYHO	Q5cni4 cryptospori
802	30	73.2	1165	2	Q7W3X5_BORPA	Q7w3x5 bordetella
803	30	73.2	1167	2	Q9RRB6_DEIRA	Q9rrb6 deinococcus
804	30	73.2	1168	2	Q7WFA5_BORBR	Q7wfa5 bordetella
805	30	73.2	1169	2	Q4RW29_TETNG	Q4rw29 tetraodon n
806	30	73.2	1218	1	MGP3_MYCPN	Q50341 mycoplasma
807	30	73.2	1226	2	Q8YI45_BRUME	Q8yi45 brucella me
808	30	73.2	1247	2	Q57CA1_BRUAB	Q57ca1 brucella ab
809	30	73.2	1247	2	Q8FZR5_BRUSU	Q8fzr5 brucella su
810	30	73.2	1319	1	SSM4_YEAST	P40318 saccharomyc
811	30	73.2	1328	2	Q61GW5_CAEER	Q61gw5 caenorhabdi
812	30	73.2	1330	2	Q22342_CAEEL	Q22342 caenorhabdi
813	30	73.2	1341	2	Q6YIH4_9CALI	Q6yih4 mink enteri

814	30	73.2	1369	2	Q6FT72_CANGA	Q6ft72 candida gla
815	30	73.2	1474	2	Q51KK4_MAGGR	Q51kk4 magnaporthe
816	30	73.2	1635	2	Q5B8N8_EMENI	Q5b8n8 aspergillus
817	30	73.2	1647	1	PQE1_CAEEL	Q10124 caenorhabdi
818	30	73.2	1783	1	RAA3_CHLRE	Q9fec4 chlamydomon
819	30	73.2	1837	2	Q584X1_9TRYP	Q584x1 trypanosoma
820	30	73.2	1872	2	Q5B7U9_EMENI	Q5b7u9 aspergillus
821	30	73.2	1893	2	Q8NJ77_EMENI	Q8nj77 emericella
822	30	73.2	1978	1	ZN638_HUMAN	Q14966 homo sapien
823	30	73.2	2539	2	Q4RMS9_TETNG	Q4rms9 tetraodon n
824	30	73.2	2938	2	Q61769_MOUSE	Q61769 mus musculu
825	30	73.2	5442	2	Q618Q0_CAEBR	Q618q0 caenorhabdi
826	30	73.2	7420	2	Q5RHP7_BRARE	Q5rhp7 brachydanio
827	29.5	72.0	1573	2	Q4RRE3_TETNG	Q4rre3 tetraodon n
828	29	70.7	31	2	Q4SRF7_TETNG	Q4srf7 tetraodon n
829	29	70.7	67	2	Q8VN56_HELPY	Q8vn56 helicobacte
830	29	70.7	67	2	Q8VN58_HELPY	Q8vn58 helicobacte
831	29	70.7	67	2	Q8VN60_HELPY	Q8vn60 helicobacte
832	29	70.7	70	2	Q4TID6_TETNG	Q4tid6 tetraodon n
833	29	70.7	96	1	Y3356_SHEON	Q8eby9 shewanella
834	29	70.7	100	2	Q43535_LILLO	Q43535 lilium long
835	29	70.7	104	2	Q86IK1_DICDI	Q86ik1 dictyosteli
836	29	70.7	110	2	Q9YFY6_AERPE	Q9yfy6 aeropyrum p
837	29	70.7	112	1	VP12_BPAPS	Q9tlt6 bacterioph
838	29	70.7	117	2	Q51PR6_MAGGR	Q51pr6 magnaporthe
839	29	70.7	117	2	Q57Y88_9TRYP	Q57y88 trypanosoma
840	29	70.7	122	2	Q517W1_ENTHI	Q517w1 entamoeba h
841	29	70.7	124	2	Q9SJJ4_ARATH	Q9sjj4 arabidopsis
842	29	70.7	133	2	Q84RM3_9LAMI	Q84rm3 boea crassi
843	29	70.7	134	2	Q4YFS3_PLABE	Q4yfs3 plasmodium
844	29	70.7	135	2	Q7MSE8_WOLSU	Q7mse8 wolinnella s
845	29	70.7	137	2	Q7WYG7_BACTU	Q7wyg7 bacillus th
846	29	70.7	146	2	Q4PKB1_9BACT	Q4pkb1 uncultured
847	29	70.7	148	2	Q55NB9_CRYNE	Q55nb9 cryptococcu
848	29	70.7	148	2	Q5KBQ4_CRYNE	Q5kbq4 cryptococcu
849	29	70.7	149	2	Q6N1U4_RHOPA	Q6nlu4 rhodopseudo
850	29	70.7	152	2	Q4PBH2_USTMA	Q4pbh2 ustilago ma
851	29	70.7	154	2	Q8ETQ5_OCEIH	Q8etq5 oceanobacil
852	29	70.7	154	2	Q7T7V5_HPBOV	Q7t7v5 hepatitis b
853	29	70.7	154	2	Q4SG22_TETNG	Q4sg22 tetraodon n
854	29	70.7	155	2	Q4V4L6_DROME	Q4v4l6 drosophila
855	29	70.7	161	2	Q4HBG8_9DEIO	Q4hbg8 deinococcus
856	29	70.7	161	2	Q5LXH2_SILPO	Q5lxh2 silicibacte
857	29	70.7	162	2	Q5NZW1_AZOSE	Q5nzw1 azoarcus sp
858	29	70.7	165	2	Q4VT14_PINRO	Q4vt14 pinus roxbu
859	29	70.7	173	2	Q82319_9DELA	Q82319 human t-lym
860	29	70.7	174	2	Q7RC70_PLAYO	Q7rc70 plasmodium
861	29	70.7	174	2	Q4XS92_PLACH	Q4xs92 plasmodium
862	29	70.7	175	2	Q7PB75_RICSI	Q7pb75 rickettsia
863	29	70.7	175	2	Q4UKP6_RICFE	Q4ukp6 rickettsia
864	29	70.7	175	2	Q92IT3_RICCN	Q92it3 rickettsia
865	29	70.7	177	1	FIMI_SALTI	Q08456 salmonella
866	29	70.7	177	1	FIMI_SALTY	P37922 salmonella
867	29	70.7	177	2	Q57S22_SALCH	Q57s22 salmonella
868	29	70.7	177	2	Q5PCD2_SALPA	Q5pcd2 salmonella
869	29	70.7	177	2	Q65QX0_MANSN	Q65qx0 mannheimia
870	29	70.7	177	2	Q98N42_RHILO	Q98n42 rhizobium 1

871	29	70.7	179	2	Q4TCE7_TETNG	Q4tce7 tetraodon n
872	29	70.7	180	2	O25756_HELPY	O25756 helicobacte
873	29	70.7	180	2	Q9ZK78_HELPJ	Q9zk78 helicobacte
874	29	70.7	182	2	Q5Z414_ORYSA	Q5z414 oryza sativ
875	29	70.7	185	2	Q4YGV8_PLABE	Q4ygv8 plasmodium
876	29	70.7	187	1	FMK1_ECOLI	P04740 escherichia
877	29	70.7	187	2	Q47442_ECOLI	Q47442 escherichia
878	29	70.7	188	2	Q7XRQ3_ORYSA	Q7xrq3 oryza sativ
879	29	70.7	190	2	Q9VJF5_DROME	Q9vjf5 drosophila
880	29	70.7	191	2	Q4YWY8_PLABE	Q4ywy8 plasmodium
881	29	70.7	194	2	Q8VR35_ECOLI	Q8vr35 escherichia
882	29	70.7	196	2	Q9V092_PYRAB	Q9v092 pyrococcus
883	29	70.7	196	2	Q619H1_CAEBR	Q619h1 caenorhabdi
884	29	70.7	198	2	Q8FAQ2_ECOL6	Q8faq2 escherichia
885	29	70.7	200	2	Q8G3I4_BIFLO	Q8g3i4 bifidobacte
886	29	70.7	205	2	Q8FNW2_COREF	Q8fnw2 corynebacte
887	29	70.7	214	2	Q9VTR5_DROME	Q9vtr5 drosophila
888	29	70.7	215	2	Q4P6H4_USTMA	Q4p6h4 ustilago ma
889	29	70.7	217	2	Q5BBH8_EMENI	Q5bbh8 aspergillus
890	29	70.7	227	1	6PGL_HELPJ	Q9zkb1 helicobacte
891	29	70.7	227	1	6PGL_HELPY	O25730 helicobacte
892	29	70.7	228	2	Q55KV8_CRYNE	Q55kv8 cryptococcu
893	29	70.7	228	2	Q5KAM1_CRYNE	Q5kam1 cryptococcu
894	29	70.7	228	2	Q7N208_PHOLL	Q7n208 photorhabdu
895	29	70.7	229	1	YXDJ_BACSU	P42421 bacillus su
896	29	70.7	231	2	Q7QP64_GIALA	Q7qp64 giardia lam
897	29	70.7	233	2	Q994E0_9ADEN	Q994e0 porcine ade
898	29	70.7	236	2	Q7PEZ5_ANOGA	Q7pez5 anopheles g
899	29	70.7	236	2	Q9VDW1_DROME	Q9vdw1 drosophila
900	29	70.7	237	2	Q7RY41_NEUCR	Q7ry41 neurospora
901	29	70.7	237	2	Q4UQ49_XANCP	Q4uq49 xanthomonas
902	29	70.7	237	2	Q8P4J4_XANCP	Q8p4j4 xanthomonas
903	29	70.7	238	1	TRY5_AEDAE	P29787 aedes aegyp
904	29	70.7	241	1	COAT_CSMV	P14985 chloris str
905	29	70.7	245	2	Q4V480_DROME	Q4v480 drosophila
906	29	70.7	247	2	Q57D77_BRUAB	Q57d77 brucella ab
907	29	70.7	247	2	Q8G0N5_BRUSU	Q8g0n5 brucella su
908	29	70.7	247	2	Q8YH72_BRUME	Q8yh72 brucella me
909	29	70.7	248	2	Q5AVL5_EMENI	Q5avl5 aspergillus
910	29	70.7	249	2	Q8GB97_HELMO	Q8gb97 heliobacill
911	29	70.7	251	2	Q5BCG0_EMENI	Q5bcg0 aspergillus
912	29	70.7	251	2	Q859I5_9CAUD	Q859i5 staphylococ
913	29	70.7	251	2	Q859K7_9CAUD	Q859k7 staphylococ
914	29	70.7	251	2	Q4ZE60_9CAUD	Q4ze60 bacterioph
915	29	70.7	251	2	Q741B8_MYCPA	Q741b8 mycobacteri
916	29	70.7	253	2	Q4WMQ8_ASPFU	Q4wmq8 aspergillus
917	29	70.7	254	2	Q5MG80_9MONO	Q5mg80 human metap
918	29	70.7	254	2	Q6QQI2_9MONO	Q6qqi2 human metap
919	29	70.7	254	2	Q6WB99_9MONO	Q6wb99 human metap
920	29	70.7	254	2	Q8AZ24_9MONO	Q8az24 human metap
921	29	70.7	254	2	Q91F56_9MONO	Q91f56 human metap
922	29	70.7	256	2	Q7RCH1_PLAYO	Q7rch1 plasmodium
923	29	70.7	262	2	Q9HVE1_PSEAE	Q9hve1 pseudomonas
924	29	70.7	266	2	Q8J231_ALTAL	Q8j231 alternaria
925	29	70.7	266	2	Q8CUZ2_OCEIH	Q8cuz2 oceanobacil
926	29	70.7	269	2	Q4YZX3_PLABE	Q4yzx3 plasmodium
927	29	70.7	272	2	Q62K09_BURMA	Q62k09 burkholderi

928	29	70.7	272	2	Q63UN8_BURPS	Q63un8 burkholderi
929	29	70.7	273	2	Q4LM62_9BURK	Q4lm62 burkholderi
930	29	70.7	276	2	Q9LYM4_ARATH	Q9lym4 arabidopsis
931	29	70.7	278	2	Q9V7Z9_DROME	Q9v7z9 drosophila
932	29	70.7	279	2	Q7NWM4_CHRVO	Q7nwm4 chromobacte
933	29	70.7	280	2	Q4V0S4_XANCP	Q4v0s4 xanthomonas
934	29	70.7	280	2	Q8PEH1_XANCP	Q8peh1 xanthomonas
935	29	70.7	282	2	Q4RYQ4_TETNG	Q4ryq4 tetraodon n
936	29	70.7	285	2	Q41603_TRITU	Q41603 triticum tu
937	29	70.7	286	2	Q20612_CAEEL	Q20612 caenorhabdi
938	29	70.7	287	2	Q7R9U3_PLAYO	Q7r9u3 plasmodium
939	29	70.7	288	2	Q4LNV7_9BURK	Q4lnv7 burkholderi
940	29	70.7	290	2	Q728C0_DESVH	Q728c0 desulfovibr
941	29	70.7	292	2	Q4NI68_9MICC	Q4ni68 arthrobacte
942	29	70.7	292	2	Q8FBW2_ECOL6	Q8fbw2 escherichia
943	29	70.7	292	2	Q83IZ6_SHIFL	Q83iz6 shigella fl
944	29	70.7	294	2	Q93JD8_STRCO	Q93jd8 streptomyce
945	29	70.7	297	2	Q8E9B9_SHEON	Q8e9b9 shewanella
946	29	70.7	304	2	Q9XU51_CAEEL	Q9xu51 caenorhabdi
947	29	70.7	305	2	Q6FFC6_ACIAD	Q6ffc6 acinetobact
948	29	70.7	306	2	Q8YYI6_ANASP	Q8yyi6 anabaena sp
949	29	70.7	307	2	Q9KKP7_VIBCH	Q9kkp7 vibrio chol
950	29	70.7	308	2	Q9BLF5_9UROC	Q9blf5 oikopleura
951	29	70.7	309	2	Q63N33_BURPS	Q63n33 burkholderi
952	29	70.7	311	2	Q5ASI9_EMENI	Q5asi9 aspergillus
953	29	70.7	311	2	Q9ZH34_ENTGE	Q9zh34 enterobacte
954	29	70.7	313	2	Q88I05_PSEPK	Q88i05 pseudomonas
955	29	70.7	314	2	Q8VIU6_MYCTU	Q8viu6 mycobacteri
956	29	70.7	317	2	Q87NU8_VIBPA	Q87nu8 vibrio para
957	29	70.7	320	2	Q8RMK7_AZOB	Q8rmk7 azospirillu
958	29	70.7	321	2	Q51F86_ENTHI	Q51f86 entamoeba h
959	29	70.7	322	2	Q7VGZ5_HELHP	Q7vgz5 helicobacte
960	29	70.7	323	2	Q9LWC0_ARATH	Q9lwc0 arabidopsis
961	29	70.7	324	2	Q9NJ18_CERCA	Q9nj18 ceratitidis c
962	29	70.7	325	2	Q9UWY5_SULSO	Q9uwy5 sulfolobus
963	29	70.7	328	2	Q5V3B6_HALMA	Q5v3b6 haloarcula
964	29	70.7	328	2	Q5APF5_CANAL	Q5apf5 candida alb
965	29	70.7	329	2	Q7S652_NEUCR	Q7s652 neurospora
966	29	70.7	333	2	Q8YLF3_ANASP	Q8ylf3 anabaena sp
967	29	70.7	339	2	Q5NHZ9_FRATT	Q5nhz9 francisella
968	29	70.7	343	2	Q4SDN9_TETNG	Q4sdn9 tetraodon n
969	29	70.7	345	2	Q4YQT9_PLABE	Q4yqt9 plasmodium
970	29	70.7	345	2	Q66098_9TOMB	Q66098 carnation r
971	29	70.7	346	2	Q8ZWZ0_PYRAE	Q8zww0 pyrobaculum
972	29	70.7	346	2	Q54JH8_DICDI	Q54jh8 dictyosteli
973	29	70.7	354	2	Q86DT4_9DIPT	Q86dt4 drosophila
974	29	70.7	356	2	Q762D2_CAMSI	Q762d2 camellia si
975	29	70.7	358	2	Q7XQM9_ORYSA	Q7xqm9 oryza sativ
976	29	70.7	361	2	Q63LI4_BURPS	Q63li4 burkholderi
977	29	70.7	361	2	Q7NR22_CHRVO	Q7nr22 chromobacte
978	29	70.7	366	2	Q54RR1_DICDI	Q54rr1 dictyosteli
979	29	70.7	367	2	Q64193_9MURI	Q64193 rattus sp.
980	29	70.7	370	2	Q83FF2_TROWT	Q83ff2 tropheryma
981	29	70.7	370	2	Q83H69_TROW8	Q83h69 tropheryma
982	29	70.7	372	2	Q93Q33_9ENTR	Q93q33 salmonella
983	29	70.7	377	2	Q7NPJ5_GLOVI	Q7npj5 gloeobacter
984	29	70.7	381	2	Q8I4M1_CAEEL	Q8i4m1 caenorhabdi

985	29	70.7	385	2	Q6G5R5_BARHE	Q6g5r5 bartonella
986	29	70.7	386	2	Q9VP20_DROME	Q9vp20 drosophila
987	29	70.7	386	2	Q9TVX6_DROME	Q9tvx6 drosophila
988	29	70.7	386	2	Q9RRZ5_DEIRA	Q9rrz5 deinococcus
989	29	70.7	389	2	Q8FQR5_COREF	Q8fqr5 corynebacte
990	29	70.7	390	2	Q8LHA1_ORYSA	Q8lha1 oryza sativ
991	29	70.7	393	2	Q18880_CAEEL	Q18880 caenorhabdi
992	29	70.7	393	2	Q9X4C4_ECOLI	Q9x4c4 escherichia
993	29	70.7	395	1	LHX3_CHICK	P53412 gallus gall
994	29	70.7	395	1	LHX3_XENLA	P36200 xenopus lae
995	29	70.7	396	2	Q5KEE4_CRYNE	Q5kee4 cryptococcu
996	29	70.7	397	2	O60056_SCHPO	O60056 schizosacch
997	29	70.7	398	2	Q6Z0V1_ORYSA	Q6z0v1 oryza sativ
998	29	70.7	400	2	Q9XDP7_ACICA	Q9xdp7 acinetobact
999	29	70.7	402	2	Q55P14_CRYNE	Q55p14 cryptococcu
1000	29	70.7	402	2	Q50LB4_9DIPT	Q50lb4 drosophila

ALIGNMENTS

RESULT 1

ADNP_RAT

ID ADNP_RAT STANDARD; PRT; 823 AA.
AC Q9JKL8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Activity-dependent neuroprotector (Activity-dependent neuroprotective
DE protein).
GN Name=Adnp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dong M., Xu K., Du Y.;
RT "Complete sequence of a rat protein containing a femtomolar-activity-
RT dependent neuroprotective peptide."
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Potential transcription factor. May mediate some of the
CC neuroprotective peptide VIP-associated effects involving normal
CC growth and cancer proliferation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- INDUCTION: By the neuroprotective peptide VIP.
CC -!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
CC -!- SIMILARITY: Contains 1 homeobox DNA-binding domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF234680; AAF40431.1; -; mRNA.

DR Ensembl; ENSRNOG00000010975; Rattus norvegicus.
 DR RGD; 71030; Adnp.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZnF_C2H2; 4.
 DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
 KW Transcription; Transcription regulation; Zinc; Zinc-finger.
 FT ZN_FING 167 189 C2H2-type 1; atypical.
 FT ZN_FING 209 230 C2H2-type 2.
 FT ZN_FING 232 255 C2H2-type 3.
 FT ZN_FING 342 367 C2H2-type 4; atypical.
 FT ZN_FING 382 406 C2H2-type 5; atypical.
 FT DNA_BIND 474 534 Homeobox.
 SQ SEQUENCE 823 AA; 91335 MW; A4C4BC616052DBDF CRC64;

Query Match 100.0%; Score 41; DB 1; Length 823;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 74 NAPVSIPQ 81

RESULT 2

ADNP_MOUSE

ID ADNP_MOUSE STANDARD; PRT; 828 AA.
 AC Q9Z103;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Activity-dependent neuroprotector (Activity-dependent neuroprotective protein).
 GN Name=Adnp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 74-81.
 RC TISSUE=Brain;
 RX MEDLINE=99155106; PubMed=10037502;
 RA Bassan M., Zamostiano R., Davidson A., Pinhasov A., Giladi E.,
 RA Perl O., Bassan H., Blat C., Gibney G., Glazner G., Brenneman D.E.,
 RA Gozes I.;
 RT "Complete sequence of a novel protein containing a femtomolar-
 RT activity-dependent neuroprotective peptide."
 RL J. Neurochem. 72:1283-1293(1999).

CC -!- FUNCTION: Potential transcription factor. May mediate some of the
 CC neuroprotective peptide VIP-associated effects involving normal
 CC growth and cancer proliferation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in the brain, with a higher
 CC expression in cerebellum and hippocampus. Weakly expressed in
 CC lung, kidney and intestine, and expressed at intermediate level in
 CC testis.
 CC -!- INDUCTION: By the neuroprotective peptide VIP.
 CC -!- MISCELLANEOUS: When isolated from the sequence, the
 CC neuroprotective peptide provides neuroprotection at subfemtomolar
 CC concentrations against toxicity associated with tetrodotoxin
 CC (electrical blockade), the beta-amyloid peptide (the Alzheimer's
 CC disease neurotoxin), N-methyl-aspartate (excitotoxicity), and the
 CC human immunodeficiency virus (HIV) envelope protein.
 CC -!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 homeobox DNA-binding domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF068198; AAD19843.1; -; mRNA.
 DR Ensembl; ENSMUSG00000051149; Mus musculus.
 DR MGI; MGI:1338758; Adnp.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZnF_C2H2; 4.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
 KW Transcription; Transcription regulation; Zinc; Zinc-finger.
 FT ZN_FING 166 188 C2H2-type 1; atypical.
 FT ZN_FING 208 229 C2H2-type 2.
 FT ZN_FING 231 254 C2H2-type 3.
 FT ZN_FING 341 366 C2H2-type 4; atypical.
 FT ZN_FING 381 405 C2H2-type 5; atypical.
 FT DNA_BIND 473 533 Homeobox.
 FT REGION 74 81 Neuroprotective peptide.
 FT COMBIAS 599 670 Glu-rich.
 SQ SEQUENCE 828 AA; 92063 MW; 9DFE669C506E8606 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 828;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIPQ 8
 |||||
 Db 74 NAPVSIPQ 81

RESULT 3

Q5RKY4_MOUSE

ID Q5RKY4_MOUSE PRELIMINARY; PRT; 922 AA.
AC Q5RKY4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Adnp protein (Fragment).
GN Name=Adnp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC050833; AAH50833.1; -; mRNA.
DR Ensembl; ENSMUSG00000051149; Mus musculus.
DR MGI; MGI:1338758; Adnp.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00096; zf-C2H2; 1.

DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZnF_C2H2; 5.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Zinc;
 KW Zinc-finger.
 FT NON_TER 1 1
 SQ SEQUENCE 922 AA; 102477 MW; D2AAB7491A54F82A CRC64;

Query Match 100.0%; Score 41; DB 2; Length 922;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 168 NAPVSIPQ 175

RESULT 4

Q5BL11_MOUSE

ID Q5BL11_MOUSE PRELIMINARY; PRT; 1004 AA.
 AC Q5BL11;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Adnp protein (Fragment).
 GN Name=Adnp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; BC090840; AAH90840.1; -; mRNA.
 DR Ensembl; ENSMUSG00000051149; Mus musculus.
 DR MGI; MGI:1338758; Adnp.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZnF_C2H2; 7.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Zinc;
 KW Zinc-finger.
 FT NON_TER 1 1
 SQ SEQUENCE 1004 AA; 111972 MW; 619AC85F4028E959 CRC64;

Query Match 100.0%; Score 41; DB 2; Length 1004;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 250 NAPVSIPQ 257

RESULT 5

Q6ZQ47_MOUSE

ID Q6ZQ47_MOUSE PRELIMINARY; PRT; 1089 AA.
 AC Q6ZQ47;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MKIAA0784 protein (Fragment).
 GN Name=Adnp; Synonyms=mKIAA0784;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22977043; PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohara O., Koga H.;

RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK129214; BAC98024.1; -; mRNA.
DR Ensembl; ENSMUSG00000051149; Mus musculus.
DR MGI; MGI:1338758; Adnp.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00355; ZnF_C2H2; 8.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Zinc;
KW Zinc-finger.
FT NON_TER 1 1
SQ SEQUENCE 1089 AA; 122153 MW; 7FF389C7FAEDF660 CRC64;

Query Match 100.0%; Score 41; DB 2; Length 1089;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
|||||||
Db 335 NAPVSIPO 342

RESULT 6

ADNP_HUMAN

ID ADNP_HUMAN STANDARD; PRT; 1102 AA.
AC Q9H2P0; O94881; Q9UG34;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Activity-dependent neuroprotector (Activity-dependent neuroprotective
DE protein).
GN Name=ADNP; Synonyms=KIAA0784;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX PubMed=11013255; DOI=10.1074/jbc.M007416200;
RA Zamostiano R., Pinhasov A., Gelber E., Steingart R.A., Seroussi E.,

RA Giladi E., Bassan M., Wollman Y., Eyre H.J., Mulley J.C.,
 RA Brenneman D.E., Gozes I.;
 RT "Cloning and characterization of the human activity-dependent
 RT neuroprotective protein.";
 RL J. Biol. Chem. 276:708-714(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehvaeslaiho M.H., Liversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 30-1102.
 RC TISSUE=Brain;
 RX MEDLINE=99087487; PubMed=9872452;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XI.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:277-286(1998).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 98-1102.
 RC TISSUE=Uterus;
 RG The German cDNA consortium;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Potential transcription factor. May mediate some of the
 CC neuroprotective peptide VIP-associated effects involving normal
 CC growth and cancer proliferation.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in heart,
 CC skeletal muscle, kidney and placenta. In brain, expression is
 CC stronger in the cerebellum and cortex regions. No expression

CC detected in the colon. Strong increase of expression in colon and
 CC breast cancer tissues.
 CC -!- SIMILARITY: Contains 9 C2H2-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 homeobox DNA-binding domain.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF250860; AAG47651.1; -; mRNA.
 DR EMBL; AL034553; CAB53748.2; -; Genomic_DNA.
 DR EMBL; AB018327; BAA34504.1; -; mRNA.
 DR EMBL; AL080163; CAB45752.1; -; mRNA.
 DR PIR; T12546; T12546.
 DR Ensembl; ENSG00000101126; Homo sapiens.
 DR HGNC; HGNC:15766; ADNP.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; ZnF_C2H2; 8.
 DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat;
 KW Transcription; Transcription regulation; Zinc; Zinc-finger.
 FT ZN_FING 74 97 C2H2-type 1.
 FT ZN_FING 107 129 C2H2-type 2; atypical.
 FT ZN_FING 165 188 C2H2-type 3.
 FT ZN_FING 221 244 C2H2-type 4.
 FT ZN_FING 447 469 C2H2-type 5; atypical.
 FT ZN_FING 489 510 C2H2-type 6; atypical.
 FT ZN_FING 512 535 C2H2-type 7.
 FT ZN_FING 622 647 C2H2-type 8; atypical.
 FT ZN_FING 662 686 C2H2-type 9; atypical.
 FT DNA_BIND 754 814 Homeobox.
 SQ SEQUENCE 1102 AA; 123563 MW; 4132E3EF814AF43B CRC64;

Query Match 100.0%; Score 41; DB 1; Length 1102;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 354 NAPVSIPQ 361

RESULT 7
 Q5BKU2_HUMAN
 ID Q5BKU2_HUMAN PRELIMINARY; PRT; 1102 AA.
 AC Q5BKU2;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE ADNP protein.
 GN Name=ADNP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RA Director MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; BC090933; AAH90933.1; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003439; ABC_transp_like.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; Znf_C2H2; 8.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Zinc;
 KW Zinc-finger.

SQ SEQUENCE 1102 AA; 123563 MW; 4132E3EF814AF43B CRC64;

Query Match 100.0%; Score 41; DB 2; Length 1102;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||
Db 354 NAPVSIPQ 361

RESULT 8

Q6DHZ8_HUMAN

ID Q6DHZ8_HUMAN PRELIMINARY; PRT; 1102 AA.
AC Q6DHZ8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Activity-dependent neuroprotector.
GN Name=ADNP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC075794; AAH75794.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003439; ABC_transp_like.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00355; Znf_C2H2; 8.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 KW DNA-binding; Homeobox; Metal-binding; Nuclear protein; Repeat; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 1102 AA; 123447 MW; 2B6984E554DC766A CRC64;

Query Match 100.0%; Score 41; DB 2; Length 1102;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||
 Db 354 NAPVSIPQ 361

RESULT 9

Q6C9B5_YARLI

ID Q6C9B5_YARLI PRELIMINARY; PRT; 445 AA.
 AC Q6C9B5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to DEHA0D16797g *Debaryomyces hansenii*.
 GN OrderedLocusNames=YALI0D12496g;
 OS *Yarrowia lipolytica* (*Candida lipolytica*).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; *Yarrowia*.
 OX NCBI_TaxID=4952;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382130; CAG80935.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 445 AA; 50191 MW; DB039F405D2D9BBC CRC64;

Query Match 87.8%; Score 36; DB 2; Length 445;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| :| | | |
Db 310 NTPISIPQ 317

RESULT 10

Q82YW3_ENTFA

ID Q82YW3_ENTFA PRELIMINARY; PRT; 470 AA.
AC Q82YW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Citrate lyase, alpha subunit.
GN Name=citF; OrderedLocusNames=EF3319;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074(2003).
DR EMBL; AE016957; AAO82984.1; -; Genomic_DNA.
DR TIGR; EF3319; -.
DR GO; GO:0009346; C:citrate lyase complex; IEA.
DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR InterPro; IPR006472; CitF.
DR Pfam; PF04223; CitF; 1.
DR PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
DR TIGRFAMs; TIGR01584; citF; 1.
KW Complete proteome.
SQ SEQUENCE 470 AA; 50138 MW; 80B3116774432C93 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
| : | | |
Db 175 NTPISIPQ 182

RESULT 11

Q8E338_STR3
ID Q8E338_STR3 PRELIMINARY; PRT; 481 AA.
AC Q8E338;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gbs1925.
GN OrderedLocusNames=gbs1925;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766854; CAD47584.1; -; Genomic_DNA.
DR SagaList; gbs1925; -.
DR InterPro; IPR006270; Strep_his_triad.
DR Pfam; PF04270; Strep_his_triad; 4.
DR TIGRFAMS; TIGR01363; strep_his_triad; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 53326 MW; DFDF0453D8A929BE CRC64;

Query Match 87.8%; Score 36; DB 2; Length 481;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
| | | : | | | :
Db 281 NAPISIPR 288

RESULT 12

Q5XC32_STRP6
ID Q5XC32_STRP6 PRELIMINARY; PRT; 510 AA.
AC Q5XC32;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Citrate lyase alpha chain (EC 4.1.3.6) (EC 2.8.3.10).
GN OrderedLocusNames=M6_Spy0896;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.
 OX NCBI_TaxID=301450;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MGAS10394;
 RX PubMed=15272401; DOI=10.1086/422697;
 RA Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Philips L.E.,
 RA Voyich J.M., DeLeo F.R., Martin J.M., Somerville G.A., Musser J.M.;
 RT "Progress toward characterization of the group A Streptococcus
 RT metagenome: complete genome sequence of a macrolide-resistant serotype
 RT M6 strain."
 RL J. Infect. Dis. 190:727-738(2004).
 DR EMBL; CP000003; AAT87031.1; -; Genomic_DNA.
 DR GO; GO:0009346; C:citrate lyase complex; IEA.
 DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006472; CitF.
 DR InterPro; IPR000049; ETF_beta.
 DR Pfam; PF04223; CitF; 1.
 DR PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
 DR ProDom; PD003528; ETF_beta; 1.
 DR TIGRFAMs; TIGR01584; citF; 1.
 KW Complete proteome; Lyase; Transferase.
 SQ SEQUENCE 510 AA; 54873 MW; A9FC17A43E67F639 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | :| | | |
 Db 215 NTPISIPQ 222

RESULT 13

Q99ZK7_STRPY
 ID Q99ZK7_STRPY PRELIMINARY; PRT; 510 AA.
 AC Q99ZK7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative citrate lyase, alpha subunit (EC 4.1.3.6).
 GN Name=citF; OrderedLocusNames=SPY1189;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
 RT "Complete genome sequence of an M1 strain of *Streptococcus pyogenes*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL; AE006559; AAK34053.1; -; Genomic_DNA.
 DR GO; GO:0009346; C:citrate lyase complex; IEA.
 DR GO; GO:0008815; F:citrate (pro-3S)-lyase activity; IEA.
 DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
 DR InterPro; IPR006472; CitF.
 DR Pfam; PF04223; CitF; 1.
 DR PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
 DR TIGRFAMs; TIGR01584; citF; 1.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 510 AA; 54990 MW; 459833B693E2EFA7 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAPVSIPO 8
 | | : | | | |
 Db 215 NTPISIPQ 222

RESULT 14

Q8P0Z3_STRP8

ID Q8P0Z3_STRP8 PRELIMINARY; PRT; 510 AA.
 AC Q8P0Z3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative citrate lyase, alpha subunit.
 GN Name=citF; OrderedLocusNames=spyM18_1140;
 OS *Streptococcus pyogenes* (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=301451;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A *Streptococcus* strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 DR EMBL; AE010039; AAL97760.1; -; Genomic_DNA.
 DR GO; GO:0009346; C:citrate lyase complex; IEA.
 DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.

DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006472; CitF.
 DR InterPro; IPR000049; ETF_beta.
 DR Pfam; PF04223; CitF; 1.
 DR PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
 DR ProDom; PD003528; ETF_beta; 1.
 DR TIGRFAMs; TIGR01584; citF; 1.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 510 AA; 54918 MW; 05F3E30FD0BAD4DF CRC64;

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | | : | | | |
 Db 215 NTPISIPQ 222

RESULT 15

Q8K7F1_STRP3

ID Q8K7F1_STRP3 PRELIMINARY; PRT; 510 AA.
 AC Q8K7F1; Q79X56;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Putative citrate lyase, alpha subunit.
 GN Name=citF; OrderedLocusNames=SPs1034, SpyM3_0834;
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=301448;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
 RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SSI-1 / Serotype M3;
 RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution.";
 RL Genome Res. 13:1042-1055(2003).
 DR EMBL; AE014153; AAM79441.1; -; Genomic_DNA.
 DR EMBL; BA000034; BAC64129.1; -; Genomic_DNA.

DR GO; GO:0009346; C:citrate lyase complex; IEA.
 DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006472; CitF.
 DR InterPro; IPR000049; ETF_beta.
 DR Pfam; PF04223; CitF; 1.
 DR ProDom; PD003528; ETF_beta; 1.
 DR TIGRFAMs; TIGR01584; citF; 1.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 510 AA; 54890 MW; F84036E9F2B0D9A8 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 510;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAPVSIPO 8
 | | : | | | |
 Db 215 NTPISIPQ 222

RESULT 16

Q8DUC1_STRMU

ID Q8DUC1_STRMU PRELIMINARY; PRT; 511 AA.
 AC Q8DUC1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative citrate lyase, alfa subunit (EC 4.1.3.6).
 GN Name=cilA; OrderedLocusNames=SMU.1021;
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UA159 / ATCC 700610 / Serotype c;
 RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
 RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
 RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
 RA Ferretti J.J.;
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 RT pathogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
 DR EMBL; AE014941; AAN58721.1; -; Genomic_DNA.
 DR GO; GO:0009346; C:citrate lyase complex; IEA.
 DR GO; GO:0008815; F:citrate (pro-3S)-lyase activity; IEA.
 DR GO; GO:0008814; F:citrate CoA-transferase activity; IEA.
 DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
 DR InterPro; IPR006472; CitF.
 DR Pfam; PF04223; CitF; 1.
 DR PIRSF; PIRSF009451; Citrt_lyas_alpha; 1.
 DR TIGRFAMs; TIGR01584; citF; 1.
 KW Complete proteome.

SQ SEQUENCE 511 AA; 55455 MW; FF966EB258334174 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 511;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | | |
Db 215 NTPISIPQ 222

RESULT 17

Q9I2G3_PSEAE

ID Q9I2G3_PSEAE PRELIMINARY; PRT; 631 AA.
AC Q9I2G3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PA1941;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004620; AAG05329.1; -; Genomic_DNA.
DR PIR; B83404; B83404.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR009056; Cyt_c_monohaem.
DR PROSITE; PS51007; CYTC; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 631 AA; 70904 MW; E72A4692AE EB75F1 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 631;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | | | | |
Db 263 NAPVSYPQ 270

RESULT 18

Q4M171_9BURK

ID Q4M171_9BURK PRELIMINARY; PRT; 707 AA.
AC Q4M171;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE TonB-dependent siderophore receptor precursor.
GN ORFNames=Bcen2424DRAFT_6742;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000001; EAM21840.1; -; Genomic_DNA.
KW Receptor; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 707 AA; 76886 MW; 3DA0B42015E0A5BF CRC64;

Query Match 87.8%; Score 36; DB 2; Length 707;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
| |||:|
Db 604 NVPVSVPO 611

RESULT 19

Q6KAS0_MOUSE

ID Q6KAS0_MOUSE PRELIMINARY; PRT; 1396 AA.
AC Q6KAS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MFLJ00137 protein (Fragment).
GN Name=Gemin5; Synonyms=mFLJ00137;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
 RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
 RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries.";
 RL DNA Res. 11:167-180(2004).
 DR EMBL; AK131137; BAD21387.1; -; mRNA.
 DR MGI; MGI:2449311; Gemin5.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 9.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM00320; WD40; 11.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE; PS50082; WD_REPEATS_2; 2.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER 1 1
 SQ SEQUENCE 1396 AA; 155527 MW; 1E6851D794FB06A0 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 1396;
 Best Local Similarity 75.0%; Pred. No. 3.5e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 |||||:
 Db 1314 NAPVSLPE 1321

RESULT 20

GEMI5_MOUSE
 ID GEMI5_MOUSE STANDARD; PRT; 1502 AA.
 AC Q8BX17;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Gem-associated protein 5 (Gemin5).
 GN Name=Gemin5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

CC -!- FUNCTION: The SMN complex plays an essential role in spliceosomal
CC snRNP assembly in the cytoplasm and is required for pre-mRNA
CC splicing in the nucleus.

CC -!- SUBUNIT: Part of the core SMN complex that contains SMN1, SIP1,
CC GEMIN2, GEMIN3, GEMIN4, GEMIN5, GEMIN6 and GEMIN7. Interacts
CC directly with SMN1, SNRNPB, SNRPD1, SNRPD2, SNRPD3 and SNRPE (By
CC similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear, found both in the nucleoplasm and
CC in nuclear bodies called gems (Gemini of Cajal bodies) that are
CC often in proximity to Cajal (coiled) bodies. Also found in the
CC cytoplasm (By similarity).

CC -!- SIMILARITY: Contains 13 WD repeats.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
DR EMBL; AK049216; BAC33614.1; -; mRNA.

DR Ensembl; ENSMUSG00000037275; Mus musculus.

DR MGI; MGI:2449311; Gemin5.

DR InterPro; IPR011990; TPR-like_helical.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 11.

DR PRINTS; PR00320; GPROTEINBRPT.

DR ProDom; PD000018; WD40; 1.

DR SMART; SM00320; WD40; 13.

DR PROSITE; PS00678; WD_REPEATS_1; 3.

DR PROSITE; PS50082; WD_REPEATS_2; 3.

DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

KW Coiled coil; mRNA processing; mRNA splicing; Nuclear protein;
KW Phosphorylation; Repeat; Spliceosome; WD repeat.
FT REPEAT 62 104 WD 1.
FT REPEAT 107 148 WD 2.
FT REPEAT 150 189 WD 3.
FT REPEAT 193 264 WD 4.
FT REPEAT 280 321 WD 5.
FT REPEAT 333 374 WD 6.
FT REPEAT 377 417 WD 7.
FT REPEAT 424 464 WD 8.
FT REPEAT 468 509 WD 9.
FT REPEAT 533 573 WD 10.
FT REPEAT 576 622 WD 11.
FT REPEAT 637 677 WD 12.
FT REPEAT 680 720 WD 13.
FT COILED 1355 1382 Potential.
FT COMBIAS 738 746 Poly-Lys.
FT MOD_RES 778 778 Phosphoserine (By similarity).
SQ SEQUENCE 1502 AA; 166562 MW; 46F98CCCE70E2971 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 1502;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||||:
Db 1420 NAPVSLPE 1427

RESULT 21

Q8SZD3_DROME

ID Q8SZD3_DROME PRELIMINARY; PRT; 189 AA.
AC Q8SZD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RE04191p.
GN Name=CG17288;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY070948; AAL48570.1; -; mRNA.
DR Ensembl; CG30457; Drosophila melanogaster.
DR FlyBase; FBgn0050457; CG30457.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.

DR InterPro; IPR000480; Glutelin.
DR InterPro; IPR004011; Gyr.
DR Pfam; PF02756; GYR; 1.
DR PRINTS; PR00211; GLUTELIN.
SQ SEQUENCE 189 AA; 19266 MW; 86B9A290DC7D84D0 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
|||
Db 27 APVSIPQ 33

RESULT 22

Q9V7Z8_DROME

ID Q9V7Z8_DROME PRELIMINARY; PRT; 189 AA.
AC Q9V7Z8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG30457-PA.
GN Name=CG30457; ORFNames=CG30457;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "*Drosophila melanogaster* release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.

RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003804; AAF57886.2; -; Genomic_DNA.
 DR Ensembl; CG30457; Drosophila melanogaster.
 DR FlyBase; FBgn0050457; CG30457.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR000480; Glutelin.
 DR InterPro; IPR004011; Gyr.
 DR Pfam; PF02756; GYR; 1.
 DR PRINTS; PR00211; GLUTELIN.
 SQ SEQUENCE 189 AA; 19248 MW; ED424DB8E9688581 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
 |||||
 Db 27 APVSIPQ 33

RESULT 23

Q92XP0_RHIME

ID Q92XP0_RHIME PRELIMINARY; PRT; 299 AA.
 AC Q92XP0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RA1204; ORFNames=SMA2233;
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymA.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymA megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL; AE007305; AAK65862.1; -; Genomic_DNA.
 DR PIR; D95412; D95412.
 KW Complete proteome; Hypothetical protein; Plasmid.
 SQ SEQUENCE 299 AA; 32694 MW; E9481CE6D6201A1B CRC64;

Query Match 85.4%; Score 35; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8

Db

|||||
6 APVSIPQ 12

RESULT 24

Q4K637_PSEF5

ID Q4K637_PSEF5 PRELIMINARY; PRT; 389 AA.
AC Q4K637;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cation efflux family protein.
GN ORFNames=PFL_5219;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pf-5;
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY94438.1; -; Genomic_DNA.
SQ SEQUENCE 389 AA; 41378 MW; A403B5AC855A05F8 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIPQ 8
:||||:|
Db 314 DAPVSVPO 321

RESULT 25

Q9XCF3_MYCAV

ID Q9XCF3_MYCAV PRELIMINARY; PRT; 3415 AA.
AC Q9XCF3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PstA.
GN Name=pstA;
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1764;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=2151;
 RX MEDLINE=22885473; PubMed=14523113; DOI=10.1099/mic.0.26528-0;
 RA Eckstein T.M., Belisle J.T., Inamine J.M.;
 RT "Proposed pathway for the biosynthesis of serovar-specific
 RT glycopeptidolipids in Mycobacterium avium serovar 2.";
 RL Microbiology 149:2797-2807(2003).
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 CC family.
 DR EMBL; AF143772; AAD44233.1; -; Genomic_DNA.
 DR HSSP; O30409; 1DNY.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA_adenyl_dom.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR010060; NRPS_synth.
 DR InterPro; IPR006163; Phsppanteth_bind.
 DR InterPro; IPR006162; Ppantne_S.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 5.
 DR Pfam; PF00550; PP-binding; 2.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMS; TIGR01733; AA-adenyl-dom; 2.
 DR TIGRFAMS; TIGR01720; NRPS-para261; 2.
 DR PROSITE; PS50075; ACP_DOMAIN; 2.
 DR PROSITE; PS00455; AMP_BINDING; 2.
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
 SQ SEQUENCE 3415 AA; 366427 MW; 36A13FA83638C45D CRC64;

Query Match 85.4%; Score 35; DB 2; Length 3415;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
 |||||
 Db 453 APVSIPQ 459

RESULT 26

Q740V0_MYCPA

ID Q740V0_MYCPA PRELIMINARY; PRT; 4027 AA.
 AC Q740V0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PstA.
 GN Name=pstA; OrderedLocusNames=MAP1242;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium avium complex (MAC).
 OX NCBI_TaxID=1770;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=k10;

RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE017231; AAS03559.1; -; Genomic_DNA.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0004043; F:L-aminoadipate-semialdehyde dehydrogenase a. . .; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA_adenyl_dom.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR010060; NRPS_synth.
 DR InterPro; IPR006163; Phspanteth_bind.
 DR InterPro; IPR006162; Ppantne_S.
 DR InterPro; IPR010080; Thioester_redct.
 DR Pfam; PF00501; AMP-binding; 3.
 DR Pfam; PF00668; Condensation; 4.
 DR Pfam; PF00550; PP-binding; 3.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 3.
 DR TIGRFAMs; TIGR01720; NRPS-para261; 1.
 DR TIGRFAMs; TIGR01746; Thioester-redct; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 3.
 DR PROSITE; PS00455; AMP_BINDING; 3.
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_3.
 KW Complete proteome.
 SQ SEQUENCE 4027 AA; 430482 MW; DE1D65B4BEF6A0E2 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 4027;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APVSIPQ 8
 |||||
 Db 461 APVSIPQ 467

RESULT 27

O28744_ARCFU

ID O28744_ARCFU PRELIMINARY; PRT; 136 AA.
 AC O28744;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein AF1528.
 GN OrderedLocusNames=AF1528;
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
 RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
 RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
 RA Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
 RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
 RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
 RA Woese C.R., Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE000997; AAB89720.1; -; Genomic_DNA.
 DR PIR; G69440; G69440.
 DR TIGR; AF1528; -.
 DR InterPro; IPR011642; Gate.
 DR Pfam; PF07670; Gate; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 136 AA; 14769 MW; 34FCF30D6A302774 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 75;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 ||| |:
 Db 29 NAPFSLPQ 36

RESULT 28

Q8BQB7_MOUSE

ID Q8BQB7_MOUSE PRELIMINARY; PRT; 158 AA.
 AC Q8BQB7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
 DE library, clone:D030066H24 product:fragile X mental retardation 2
 DE homolog, full insert sequence. (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK051081; BAC34520.1; -; mRNA.
 DR Ensembl; ENSMUSG00000031189; Mus musculus.
 DR InterPro; IPR007797; AF-4.
 DR Pfam; PF05110; AF-4; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 158 AA; 17828 MW; 2B094A8C3BCB3B11 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 158;
 Best Local Similarity 75.0%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | ||:||||
 Db 94 NGPVTIPQ 101

RESULT 29

Q5NIK3_FRATT

ID Q5NIK3_FRATT PRELIMINARY; PRT; 458 AA.
 AC Q5NIK3;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE ATP synthase beta chain (EC 3.6.3.14).
 GN Name=atpD; OrderedLocusNames=FTT0064;
 OS Francisella tularensis (subsp. tularensis).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
 OC Francisellaceae; Francisella.
 OX NCBI_TaxID=119856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCHU S4 / Schu 4;
 RX PubMed=15640799; DOI=10.1038/ng1499;
 RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
 RA Fuxelius H.-H., Garcia E., Haelletorp G., Johansson D., Isherwood K.E.,
 RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
 RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
 RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
 RA Titball R.W.;
 RT "The complete genome sequence of Francisella tularensis, the causative
 RT agent of tularemia.";
 RL Nat. Genet. 37:153-159(2005).
 CC -!- FUNCTION: Produces ATP from ADP in the presence of a proton
 CC gradient across the membrane. The beta chain is the catalytic
 CC subunit (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
 CC core - and CF(0) - the membrane proton channel. CF(1) has five
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
 CC has three main subunits: a, b and c (By similarity).
 DR EMBL; AJ749949; CAG44697.1; -; Genomic_DNA.

DR GO; GO:0045255; C:hydrogen-translocating F-type ATPase complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . .; IEA.
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . .; IEA.
 DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. . .; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR005722; ATP_synthF1_beta.
 DR InterPro; IPR000793; ATPase_a/b_C.
 DR InterPro; IPR004100; ATPase_a/b_N.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR Pfam; PF00306; ATP-synt_ab_C; 1.
 DR Pfam; PF02874; ATP-synt_ab_N; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR01039; atpD; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
 KW ATP synthesis; ATP-binding; CF(1); Complete proteome;
 KW Hydrogen ion transport; Hydrolase; Ion transport; Nucleotide-binding;
 KW Transport.
 SQ SEQUENCE 458 AA; 49801 MW; 5D9DC1A72D4DC706 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 458;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIP 7
 |||:|:
 Db 71 NAPISVP 77

RESULT 30

Q6FFK0_ACIAD

ID Q6FFK0_ACIAD PRELIMINARY; PRT; 464 AA.
 AC Q6FFK0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane-bound ATP synthase , F1 sector, beta-subunit
 DE (EC 3.6.3.14).
 GN Name=atpD; OrderedLocusNames=ACIAD0187;
 OS Acinetobacter sp. (strain ADP1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=62977;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ADP1;
 RX PubMed=15514110; DOI=10.1093/nar/gkh910;
 RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
 RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
 RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.
 RT ADP1, a versatile and naturally transformation competent bacterium.";

RL Nucleic Acids Res. 32:5766-5779(2004).
 DR EMBL; CR543861; CAG67157.1; -; Genomic_DNA.
 DR GO; GO:0045255; C:hydrogen-translocating F-type ATPase complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . .; IEA.
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . .; IEA.
 DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. . .; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR InterPro; IPR000793; ATPase_a/b_C.
 DR InterPro; IPR004100; ATPase_a/b_N.
 DR InterPro; IPR005722; ATP_synthF1_beta.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR Pfam; PF00306; ATP-synt_ab_C; 1.
 DR Pfam; PF02874; ATP-synt_ab_N; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR01039; atpD; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 464 AA; 50311 MW; 61018A15C4AB3534 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 464;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIP 7
 |||:|:
 Db 71 NAPISVP 77

RESULT 31

Q84LK3_ORYSA

ID Q84LK3_ORYSA PRELIMINARY; PRT; 503 AA.
 AC Q84LK3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Betaine aldehyde dehydrogenase.
 GN Name=BADH2; Synonyms=OSJNBa0056L09.30, P0456B03.101;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Asayama M.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
 DR EMBL; AP004463; BAC98555.1; -; Genomic_DNA.
 DR EMBL; AB096083; BAC76608.1; -; mRNA.
 DR EMBL; AP005537; BAC99806.1; -; Genomic_DNA.
 DR HSSP; P05091; 1004.
 DR Gramene; Q84LK3; -.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002086; Aldehyd_dehydrog.
 DR InterPro; IPR012303; NAD_ald_dehydrog.
 DR Pfam; PF00171; Aldedh; 1.
 DR PIRSF; PIRSF000147; DHA; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 503 AA; 54682 MW; 1011B305C31F4446 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 503;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 |||||:
 Db 133 NAPVSLP 139

RESULT 32

Q9V3B2_DROME

ID Q9V3B2_DROME PRELIMINARY; PRT; 505 AA.
 AC Q9V3B2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG5519-PA (BcDNA.LD02793).
 GN Name=Gbp; Synonyms=BcDNA.LD02793; ORFNames=CG5519;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M.,
 RA Lewis S.E., Suh C., Rubin G.M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- INTERACTION:
 CC Q9VJ62:CG10341; NbExp=1; IntAct=EBI-115372, EBI-154062;
 CC Q9VHB3:CG16790; NbExp=1; IntAct=EBI-115372, EBI-92020;
 DR EMBL; AE003799; AAF57684.1; -; Genomic_DNA.
 DR EMBL; AF160906; AAD46846.1; -; mRNA.
 DR HSSP; P32523; 1N87.
 DR IntAct; Q9V3B2; -.
 DR Ensembl; CG5519; Drosophila melanogaster.
 DR FlyBase; FBgn0013969; CG5519.
 DR FlyBase; FBgn0013969; Gbp.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR003613; Ubox.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR SMART; SM00504; Ubox; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
 DR PROSITE; PS50082; WD_REPEATS_2; 4.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 SQ SEQUENCE 505 AA; 55199 MW; F54CFFB8B5099FD1 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 505;
 Best Local Similarity 75.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 ||| :|||
 Db 142 NAPTAIPQ 149

RESULT 33
 Q6MAF9_PARUW
 ID Q6MAF9_PARUW PRELIMINARY; PRT; 597 AA.

AC Q6MAF9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=pc1716;
 OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
 OX NCBI_TaxID=264201;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15073324;
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rattei T., Mewes H.-W., Wagner M.;
 RT "Illuminating the evolutionary history of chlamydiae.";
 RL Science 304:728-730(2004).
 DR EMBL; BX908798; CAF24440.1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 597 AA; 67392 MW; 628BEF34975A13D7 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 597;
 Best Local Similarity 75.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | | : | | | |
 Db 529 NGPLSIPQ 536

RESULT 34

Q50YT9_ENTHI

ID Q50YT9_ENTHI PRELIMINARY; PRT; 685 AA.
 AC Q50YT9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=130.t00012;
 OS Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
 RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
 RA Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z.,
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
 RA Fraser C.M., Hall N.;

RT "The genome of the protist parasite *Entamoeba histolytica*."
 RL Nature 433:865-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFB01000447; EAL46756.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 685 AA; 76517 MW; 1C591AC9DC5CE965 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 685;
 Best Local Similarity 71.4%; Pred. No. 4.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 |||:|:
 Db 122 NAPISVP 128

RESULT 35

Q4R3H9_MACFA

ID Q4R3H9_MACFA PRELIMINARY; PRT; 946 AA.
 AC Q4R3H9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Testis cDNA clone: QtsA-16835, similar to human fragile X mental
 DE retardation 2 (FMR2),.
 OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; *Macaca*.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications."
 RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs."
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB179287; BAE02338.1; -; mRNA.
 SQ SEQUENCE 946 AA; 104544 MW; 0AB31DD05754BDBD CRC64;

Query Match 82.9%; Score 34; DB 2; Length 946;
 Best Local Similarity 75.0%; Pred. No. 6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
 | ||:|
 Db 865 NGPVTIPQ 872

RESULT 36

AFF2_MOUSE

ID AFF2_MOUSE STANDARD; PRT; 1272 AA.
AC O55112;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AF4/FMR2 family member 2 (Fragile X mental retardation protein 2
DE homolog) (Protein FMR-2) (FMR2P) (Ox19 protein).
GN Name=Aff2; Synonyms=Fmr2, Ox19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=98133924; PubMed=9467002; DOI=10.1093/hmg/7.3.441;
RA Chakrabarti L., Bristulf J., Foss G.S., Davies K.E.;
RT "Expression of the murine homologue of FMR2 in mouse brain and during
RT development.";
RL Hum. Mol. Genet. 7:441-448(1998).
CC -!- TISSUE SPECIFICITY: Highly expressed in the hippocampus, the
CC piriform cortex, Purkinje cells and the cingulate gyrus.
CC -!- DEVELOPMENTAL STAGE: Expressed before day 7 in the embryo and
CC reached its highest levels at 10.5-11.5 days. In the embryo at day
CC 11, expression is more specific in the roof of the hind brain and
CC the lateral ventricle of the brain.
CC -!- SIMILARITY: Belongs to the AF4 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ001549; CAA04821.1; -; mRNA.
DR PIR; T30248; T30248.
DR Ensembl; ENSMUSG00000031189; Mus musculus.
DR MGI; MGI:1202294; Fmr2.
DR GO; GO:0007611; P:learning and/or memory; IMP.
DR InterPro; IPR007797; AF-4.
DR Pfam; PF05110; AF-4; 1.
SQ SEQUENCE 1272 AA; 140159 MW; 2FCC4C00F5732592 CRC64;

Query Match 82.9%; Score 34; DB 1; Length 1272;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| ||:||||
Db 1191 NGPVTIPQ 1198

RESULT 37

AFF2_PANTR

ID AFF2_PANTR STANDARD; PRT; 1272 AA.
AC Q7YQM2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AF4/FMR2 family member 2 (Fragile X mental retardation protein 2
DE homolog) (Protein FMR-2).
GN Name=AFF2; Synonyms=FMR2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289(2003).
CC -!- SIMILARITY: Belongs to the AF4 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB102645; BAC81114.1; -; mRNA.
DR InterPro; IPR007797; AF-4.
DR Pfam; PF05110; AF-4; 1.
SQ SEQUENCE 1272 AA; 140509 MW; DDF13B3E11751EE4 CRC64;

Query Match 82.9%; Score 34; DB 1; Length 1272;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| ||:||||
Db 1191 NGPVTIPQ 1198

RESULT 38

AFF2_PONPY
ID AFF2_PONPY STANDARD; PRT; 1272 AA.
AC Q7YQM1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AF4/FMR2 family member 2 (Fragile X mental retardation protein 2
DE homolog) (Protein FMR-2).
GN Name=AFF2; Synonyms=FMR2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
 RA Kitano T., Schwarz C., Nickel B., Paabo S.;
 RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
 RT chimpanzees.";
 RL Mol. Biol. Evol. 20:1281-1289(2003).
 CC -!- SIMILARITY: Belongs to the AF4 family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB102646; BAC81115.1; -; mRNA.
 DR InterPro; IPR007797; AF-4.
 DR Pfam; PF05110; AF-4; 1.
 SQ SEQUENCE 1272 AA; 140637 MW; 7B87D97AF91D840D CRC64;

Query Match 82.9%; Score 34; DB 1; Length 1272;
 Best Local Similarity 75.0%; Pred. No. 8.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | ||:||||
 Db 1191 NGPVTIPQ 1198

RESULT 39

Q7Z400_HUMAN

ID Q7Z400_HUMAN PRELIMINARY; PRT; 1272 AA.
 AC Q7Z400;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE FMR2 protein.
 GN Name=FMR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
 RA Kitano T., Schwarz C., Nickel B., Paabo S.;
 RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
 RT chimpanzees.";
 RL Mol. Biol. Evol. 20:1281-1289(2003).
 DR EMBL; AB102644; BAC81113.1; -; mRNA.
 DR InterPro; IPR007797; AF-4.
 DR Pfam; PF05110; AF-4; 1.
 SQ SEQUENCE 1272 AA; 140506 MW; 15EBFC9FEF5E06B8 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 1272;
 Best Local Similarity 75.0%; Pred. No. 8.3e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| ||:|
Db 1191 NGPVTIPQ 1198

RESULT 40

AFF2_HUMAN

ID AFF2_HUMAN STANDARD; PRT; 1311 AA.
AC P51816; O43786; O60215; P78407; Q13521; Q14323; Q9UNA5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AF4/FMR2 family member 2 (Fragile X mental retardation 2 protein)
DE (Protein FMR-2) (FMR2P) (Ox19 protein) (Fragile X E mental retardation
DE syndrome protein).
GN Name=AFF2; Synonyms=FMR2, OX19;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Fetal brain, and Placenta;
RX MEDLINE=96241583; PubMed=8673085;
RA Gecz J., Gedeon A.K., Sutherland G.R., Mulley J.C.;
RT "Identification of the gene FMR2, associated with FRAXE mental
RT retardation.";
RL Nat. Genet. 13:105-108(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=96241584; PubMed=8673086;
RA Gu Y., Shen Y., Gibbs R.A., Nelson D.L.;
RT "Identification of FMR2, a novel gene associated with the FRAXE CCG
RT repeat and CpG island.";
RL Nat. Genet. 13:109-113(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RC TISSUE=Fetal brain;
RX MEDLINE=96422267; PubMed=8824884; DOI=10.1093/hmg/5.2.275;
RA Chakrabarti L., Knight S.J.L., Flannery A.V., Davies K.E.;
RT "A candidate gene for mild mental handicap at the FRAXE fragile
RT site.";
RL Hum. Mol. Genet. 5:275-282(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=97446139; PubMed=9299237; DOI=10.1006/geno.1997.4867;
RA Gecz J., Bielby S., Sutherland G.R., Mulley J.C.;
RT "Gene structure and subcellular localization of FMR2, a member of a
RT new family of putative transcription activators.";
RL Genomics 44:201-213(1997).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Brain;

RX MEDLINE=98133924; PubMed=9467002; DOI=10.1093/hmg/7.3.441;
 RA Chakrabarti L., Bristulf J., Foss G.S., Davies K.E.;
 RT "Expression of the murine homologue of FMR2 in mouse brain and during
 RT development.";
 RL Hum. Mol. Genet. 7:441-448(1998).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15772651; DOI=10.1038/nature03440;
 RA Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
 RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
 RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
 RA Jones M.C., Hurler M.E., Andrews T.D., Scott C.E., Searle S.,
 RA Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
 RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
 RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
 RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
 RA Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,
 RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
 RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
 RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
 RA Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
 RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
 RA Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
 RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
 RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
 RA Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
 RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
 RA Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
 RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
 RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
 RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
 RA Hawes A., Heath P.D., Heitmann K., Hennig S., Hernandez J.,
 RA Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
 RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
 RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
 RA Kioschis P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
 RA Laird G.K., Langford C., Lawlor S., Laversha M., Lewis L., Liu W.,
 RA Lloyd C., Lloyd D.M., Loulseged H., Loveland J.E., Lovell J.D.,
 RA Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
 RA McDowall J., McLaren S., McMurray A., Meidl P., Meitinger T.,
 RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
 RA Mullikin J.C., Nguyen N., Nordsiek G., Nyakatura G., O'dell C.N.,
 RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
 RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
 RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
 RA Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
 RA Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
 RA Smith M.L., Sotheran E.C., Steingruber H.E., Steward C.A., Storey R.,
 RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
 RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
 RA Tromans A.C., d'Urso M., Verduzco D., Villasana D., Waldron L.,
 RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
 RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
 RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
 RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
 RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,

RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
 RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
 RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
 RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
 RT "The DNA sequence of the human X chromosome."
 RL Nature 434:325-337(2005).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 348-421 (ISOFORM 1).
 RA Wang L., Thibodeau S.N.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P51816-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P51816-2; Sequence=VSP_000211, VSP_000212, VSP_000213;
 CC Name=3;
 CC IsoId=P51816-3; Sequence=VSP_000211, VSP_000212, VSP_000216;
 CC Name=4;
 CC IsoId=P51816-4; Sequence=VSP_000211, VSP_000212, VSP_000213,
 CC VSP_000214, VSP_000215;
 CC -!- TISSUE SPECIFICITY: Brain (most abundant in hippocampus and
 CC amygdala), placenta and lung.
 CC -!- DISEASE: Defects in AFF2 are the cause of FRAXE [MIM:309548].
 CC FRAXE is an X-linked form of mental retardation. Loss of FMR2
 CC expression is correlated with FRAXE CCG(N) expansion. Normal
 CC individuals have 6-35 copies of the repeat, whereas
 CC cytogenetically positive, developmentally delayed males have more
 CC than 200 copies and show methylation of the associated CPG island.
 CC -!- SIMILARITY: Belongs to the AF4 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U48436; AAC82513.1; -; mRNA.
 DR EMBL; L76569; AAA99416.1; -; mRNA.
 DR EMBL; X95463; CAA64730.1; -; mRNA.
 DR EMBL; AF012624; AAB71534.1; -; Genomic_DNA.
 DR EMBL; AF012603; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012604; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012605; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012606; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012607; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012608; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012609; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012610; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012611; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012612; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012613; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012614; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012615; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012616; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012617; AAB71534.1; JOINED; Genomic_DNA.

DR EMBL; AF012618; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012619; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012620; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012621; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012622; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AF012623; AAB71534.1; JOINED; Genomic_DNA.
 DR EMBL; AJ001550; CAA04822.1; -; mRNA.
 DR EMBL; AC005731; AAB69976.1; -; Genomic_DNA.
 DR EMBL; AC015552; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AC006516; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AC002368; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AF139979; AAD45878.1; -; Genomic_DNA.
 DR EMBL; AF139977; AAD45878.1; JOINED; Genomic_DNA.
 DR EMBL; AF139978; AAD45878.1; JOINED; Genomic_DNA.
 DR Ensembl; ENSG00000155966; Homo sapiens.
 DR HGNC; HGNC:3776; AFF2.
 DR MIM; 309548; -.
 DR GO; GO:0007420; P:brain development; TAS.
 DR InterPro; IPR007797; AF-4.
 DR Pfam; PF05110; AF-4; 1.
 KW Alternative splicing; Disease mutation; Triplet repeat expansion.
 FT VARSPLIC 57 60 Missing (in isoform 2, isoform 3 and
 FT isoform 4).
 FT /FTId=VSP_000211.
 FT VARSPLIC 364 392 Missing (in isoform 2, isoform 3 and
 FT isoform 4).
 FT /FTId=VSP_000212.
 FT VARSPLIC 416 421 Missing (in isoform 2 and isoform 4).
 FT /FTId=VSP_000213.
 FT VARSPLIC 466 466 N -> K (in isoform 4).
 FT /FTId=VSP_000214.
 FT VARSPLIC 467 1311 Missing (in isoform 4).
 FT /FTId=VSP_000215.
 FT VARSPLIC 970 971 Missing (in isoform 3).
 FT /FTId=VSP_000216.
 FT CONFLICT 195 195 D -> A (in Ref. 3).
 FT CONFLICT 470 470 A -> V (in Ref. 2).
 FT CONFLICT 548 548 P -> Q (in Ref. 5 and 6).

Query Match 82.9%; Score 34; DB 1; Length 1311;
 Best Local Similarity 75.0%; Pred. No. 8.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | ||:||||
 Db 1230 NGPVTIPQ 1237

RESULT 41
 Q8T145_DICDI
 ID Q8T145_DICDI PRELIMINARY; PRT; 1789 AA.
 AC Q8T145;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Similar to ATP-dependent RNA helicase, putative; protein id:
 DE Atlg35530.1 (Hypothetical protein).

GN ORFNames=DDB0217507;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
 RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
 RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
 RA Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 RL Nature 418:79-85(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 DR EMBL; AAFI01000027; EAL70313.1; -; Genomic_DNA.
 DR EMBL; AC117070; AAM09323.2; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR006935; ResIII.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF04851; ResIII; 1.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00490; HELICc; 1.
 KW Helicase; Hypothetical protein.
 SQ SEQUENCE 1789 AA; 201678 MW; 235BC414E1CAFDA9 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 1789;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
| | : | : | |
Db 104 NVPISLPQ 111

RESULT 42

Q8A044_BACTN

ID Q8A044_BACTN PRELIMINARY; PRT; 104 AA.
AC Q8A044;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BT4177;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016944; AAO79282.1; -; Genomic_DNA.
DR InterPro; IPR008000; DUF718.
DR Pfam; PF05336; DUF718; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 12123 MW; 348F15B6A63C7A17 CRC64;

Query Match 80.5%; Score 33; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
| : | | | | |
Db 90 NSPVSIP 96

RESULT 43

Q5CXV6_CRYPV

ID Q5CXV6_CRYPV PRELIMINARY; PRT; 129 AA.
AC Q5CXV6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE DNA-directed RNA polymerase subunit.
GN ORFNames=cgd7_4770;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Iowa type II;
 RX PubMed=15044751; DOI=10.1126/science.1094786;
 RA Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
 RA Lancto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
 RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
 RA Anantharaman V., Aravind L., Kapur V.;
 RT "Complete genome sequence of the apicomplexan, Cryptosporidium
 RT parvum.";
 RL Science 304:441-445(2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEE01000001; EAK90445.1; -; Genomic_DNA.
 DR InterPro; IPR010991; p53_tetrameristn.
 DR InterPro; IPR006111; RNA_polK_14kDa.
 DR InterPro; IPR006110; RNA_poly_Rpb6.
 DR Pfam; PF01192; RNA_pol_Rpb6; 1.
 DR PROSITE; PS01111; RNA_POL_K_14KD; 1.
 KW DNA-directed RNA polymerase.
 SQ SEQUENCE 129 AA; 14975 MW; A14758CB98757E9F CRC64;

Query Match 80.5%; Score 33; DB 2; Length 129;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIP 7
 ||||:||
 Db 79 NAPVAIP 85

RESULT 44

Q5CLN5_CRYHO
 ID Q5CLN5_CRYHO PRELIMINARY; PRT; 129 AA.
 AC Q5CLN5;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE DNA-directed RNA polymerase IIa.
 GN ORFNames=Chro.70529;
 OS Cryptosporidium hominis.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=237895;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TU502;
 RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
 RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
 RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
 RA Buck G.A.;
 RT "The genome of Cryptosporidium hominis.";
 RL Nature 431:1107-1112(2004).
 DR EMBL; AAEL01000048; EAL37521.1; -; Genomic_DNA.

DR SMR; Q5CLN5; 54-129.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006351; P:transcription, DNA-dependent; IEA.
 DR InterPro; IPR006111; RNA_polK_14kDa.
 DR InterPro; IPR006110; RNA_poly_Rpb6.
 DR Pfam; PF01192; RNA_pol_Rpb6; 1.
 DR PROSITE; PS01111; RNA_POL_K_14KD; 1.
 KW DNA-directed RNA polymerase.
 SQ SEQUENCE 129 AA; 14976 MW; A14758CB98757E9F CRC64;

Query Match 80.5%; Score 33; DB 2; Length 129;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPVSIP 7
 ||||:|
 Db 79 NAPVAIP 85

RESULT 45

Q57QN6_SALCH

ID Q57QN6_SALCH PRELIMINARY; PRT; 159 AA.
 AC Q57QN6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Trp-repressor binding protein.
 GN Name=wraB; OrderedLocusNames=SC1069;
 OS Salmonella cholerae-suis (Salmonella enterica).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=591;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC-B67;
 RX PubMed=15781495;
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
 RA Wang H.-S., Lee Y.-S.;
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
 RT highly invasive and resistant zoonotic pathogen."
 RL Nucleic Acids Res. 33:1690-1698(2005).
 DR EMBL; AE017220; AAX64975.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 159 AA; 16908 MW; 1FD7E0605234E615 CRC64;

Query Match 80.5%; Score 33; DB 2; Length 159;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 ||||:|
 Db 57 NAPVATPQ 64

RESULT 46

WRBA_SALPA

ID WRBA_SALPA STANDARD; PRT; 197 AA.
AC Q5PG91;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Flavoprotein wrbA (Trp repressor binding protein).
GN Name=wrbA; OrderedLocusNames=SPA1731;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -!- FUNCTION: Seems to enhance the formation and/or stability of
CC noncovalent complexes between the trp repressor protein and
CC operator-bearing DNA (By similarity).
CC -!- COFACTOR: Binds 1 FMN per monomer (By similarity).
CC -!- SIMILARITY: Belongs to the wrbA family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CP000026; AAV77652.1; -; Genomic_DNA.
DR HAMAP; MF_01017; -; 1.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR010089; Flav_wrbA.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR TIGRFAMs; TIGR01755; flav_wrbA; 1.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
KW Complete proteome; Flavoprotein; FMN.
FT INIT_MET 0 0 By similarity.
FT DOMAIN 3 188 Flavodoxin-like.
SQ SEQUENCE 197 AA; 20730 MW; 7FD1191F8E031610 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
|||: ||
Db 56 NAPVATPQ 63

RESULT 47

WRBA_SALTI

ID WRBA_SALTI STANDARD; PRT; 197 AA.
AC Q8Z7N9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Flavoprotein wrbA (Trp repressor binding protein).
GN Name=wrbA; OrderedLocusNames=STY1155, t1801;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Seems to enhance the formation and/or stability of
CC noncovalent complexes between the trp repressor protein and
CC operator-bearing DNA (By similarity).
CC -!- COFACTOR: Binds 1 FMN per monomer (By similarity).
CC -!- SIMILARITY: Belongs to the wrbA family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL627269; CAD08244.1; -; Genomic_DNA.
DR EMBL; AE016840; AAO69423.1; -; Genomic_DNA.
DR HAMAP; MF_01017; -; 1.
DR InterPro; IPR008254; Flav_nitox_synth.

DR InterPro; IPR010089; Flav_wrbA.
 DR InterPro; IPR001226; Flavodoxin.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR TIGRFAMS; TIGR01755; flav_wrbA; 1.
 DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
 KW Complete proteome; Flavoprotein; FMN.
 FT INIT_MET 0 0 By similarity.
 FT DOMAIN 3 188 Flavodoxin-like.
 SQ SEQUENCE 197 AA; 20706 MW; DCD65E43E98C7112 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 197;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 ||||: ||
 Db 56 NAPVATPQ 63

RESULT 48

WRBA_SALTY

ID WRBA_SALTY STANDARD; PRT; 197 AA.
 AC Q8ZQ40;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Flavoprotein wrbA (Trp repressor binding protein).
 GN Name=wrbA; OrderedLocusNames=STM1119;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: Seems to enhance the formation and/or stability of
 CC noncovalent complexes between the trp repressor protein and
 CC operator-bearing DNA (By similarity).
 CC -!- COFACTOR: Binds 1 FMN per monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the wrbA family.
 CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
 CC -----
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 CC -----

DR EMBL; AE008748; AAL20051.1; -; Genomic_DNA.
 DR StyGene; SG?????; wrbA.
 DR HAMAP; MF_01017; -; 1.
 DR InterPro; IPR008254; Flav_nitox_synth.
 DR InterPro; IPR010089; Flav_wrbA.
 DR InterPro; IPR001226; Flavodoxin.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR TIGRFAMs; TIGR01755; flav_wrbA; 1.
 DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
 KW Complete proteome; Flavoprotein; FMN.
 FT INIT_MET 0 0 By similarity.
 FT DOMAIN 3 188 Flavodoxin-like.
 SQ SEQUENCE 197 AA; 20736 MW; C52F61B136A185C6 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 197;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPO 8
 ||||: ||
 Db 56 NAPVATPQ 63

RESULT 49

HIS2_HELHP

ID HIS2_HELHP STANDARD; PRT; 231 AA.
 AC Q7VJ02;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Histidine biosynthesis bifunctional protein hisIE [Includes:
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].
 GN Name=hisI; Synonyms=hisIE; OrderedLocusNames=HH0449;
 OS Helicobacter hepaticus.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=32025;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 51449 / 3B1;
 RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
 RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
 RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
 RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
 RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
 RT "The complete genome sequence of the carcinogenic bacterium
 RT Helicobacter hepaticus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
 CC -!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-
 CC phosphoribosyl)-AMP + diphosphate.
 CC -!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-
 CC phosphoribosyl)-5-((5-
 CC phosphoribosylamino)methylideneamino)imidazole-4-carboxamide.
 CC -!- PATHWAY: Amino-acid biosynthesis; L-histidine biosynthesis; L-
 CC histidine from PRPP: step 2.
 CC -!- PATHWAY: Amino-acid biosynthesis; L-histidine biosynthesis; L-

CC histidine from PRPP: step 3.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: In the N-terminal section; belongs to the PRA-CH
 CC family.
 CC -!- SIMILARITY: In the C-terminal section; belongs to the PRA-PH
 CC family.
 CC -----
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 CC -----
 DR EMBL; AE017145; AAP77046.1; -; Genomic_DNA.
 DR HAMAP; MF_01019; -; 1.
 DR InterPro; IPR008179; PRA-PH.
 DR InterPro; IPR002496; PRA_cyclohydro.
 DR InterPro; IPR008178; Pra_PH/CH.
 DR Pfam; PF01502; PRA-CH; 1.
 DR Pfam; PF01503; PRA-PH; 1.
 DR ProDom; PD002610; PRA_cyclohydro; 1.
 DR ProDom; PD002611; Pra_PH/CH; 1.
 KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Hydrolase; Multifunctional enzyme.
 FT REGION 1 130 Phosphoribosyl-AMP cyclohydrolase.
 FT REGION 131 231 Phosphoribosyl-ATP pyrophosphohydrolase.
 SQ SEQUENCE 231 AA; 26830 MW; AB35A5FEE6E68307 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 231;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPVSIPQ 8
 | | | | : | |
 Db 114 NPPVSMPQ 121

RESULT 50

Q6W4C2_DROME
 ID Q6W4C2_DROME PRELIMINARY; PRT; 253 AA.
 AC Q6W4C2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cinnamon (Fragment).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Zim30;
 RA Sheldahl L.A., Weinreich D.M., Rand D.M.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY312722; AAQ67536.1; -; Genomic_DNA.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.

DR InterPro; IPR001453; MoCF_bios.
 DR InterPro; IPR008284; MoCF_biosynth.
 DR InterPro; IPR005110; MoeA_N.
 DR InterPro; IPR000169; Pept_cys_AS.
 DR Pfam; PF00994; MoCF_biosynth; 1.
 DR Pfam; PF03453; MoeA_N; 1.
 DR TIGRFAMs; TIGR00177; molyb_syn; 1.
 DR PROSITE; PS01078; MOCF_BIOSYNTHESIS_1; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 253 253
 SQ SEQUENCE 253 AA; 27611 MW; 34069E6F21EE62ED CRC64;

Query Match 80.5%; Score 33; DB 2; Length 253;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPVSIP 7
 ||||:||
 Db 215 NAPVNIP 221

Search completed: April 26, 2006, 00:22:23
 Job time : 271 secs